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OM protein - protein search, using sw model

Run on: February 4, 2003, 12:56:41 ; Search time 15.4575 Seconds
(without alignments)
315.977 Million cell updates/sec

Title: US-09-854-864-15

Perfect score: 909
Sequence: 1 MSGIGRSRRGGRSRVDQER.....SPALPGIKLSADQVALVYST 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/Backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-------------------|--------------------|
| 1 | 909 | 100.0 | 166 | US-08-810-572A-6 | Sequence 6, Appli |
| 2 | 909 | 100.0 | 166 | US-09-290-333-6 | Sequence 6, Appli |
| 3 | 909 | 100.0 | 293 | US-08-810-572A-2 | Sequence 2, Appli |
| 4 | 909 | 100.0 | 293 | US-09-290-333-2 | Sequence 2, Appli |
| 5 | 82.5 | 9.1 | 799 | US-08-525-940-23 | Sequence 23, Appli |
| 6 | 82.5 | 9.1 | 799 | US-08-525-940-23 | Sequence 23, Appli |
| 7 | 82.5 | 9.1 | 881 | US-08-525-940-21 | Sequence 21, Appli |
| 8 | 82.5 | 9.1 | 881 | US-08-525-940-21 | Sequence 21, Appli |
| 9 | 82.5 | 9.1 | 915 | US-08-525-940-18 | Sequence 18, Appli |
| 10 | 82.5 | 9.1 | 915 | US-08-525-940-18 | Sequence 18, Appli |
| 11 | 82.5 | 9.1 | 915 | US-09-214-555B-2 | Sequence 2, Appli |
| 12 | 82.5 | 9.1 | 915 | US-09-214-555B-2 | Sequence 2, Appli |
| 13 | 81 | 8.9 | 704 | US-09-590-656-2 | Sequence 2, Appli |
| 14 | 81 | 8.9 | 977 | US-09-590-656-1 | Sequence 1, Appli |
| 15 | 81 | 8.9 | 1124 | US-08-323-474-2 | Sequence 2, Appli |
| 16 | 81 | 8.9 | 1124 | US-08-323-474-2 | Sequence 2, Appli |
| 17 | 79.5 | 8.7 | 98 | US-08-465-380-21 | Sequence 21, Appli |
| 18 | 79.5 | 8.7 | 98 | US-08-465-380-21 | Sequence 21, Appli |
| 19 | 79.5 | 8.7 | 98 | US-08-480-478-49 | Sequence 49, Appli |
| 20 | 79.5 | 8.7 | 98 | US-08-486-397-21 | Sequence 21, Appli |
| 21 | 79.5 | 8.7 | 98 | US-08-486-397-21 | Sequence 21, Appli |
| 22 | 79.5 | 8.7 | 98 | US-08-461-965-21 | Sequence 21, Appli |
| 23 | 79.5 | 8.7 | 98 | US-08-326-110A-49 | Sequence 49, Appli |
| 24 | 79.5 | 8.7 | 98 | US-08-634-641-21 | Sequence 21, Appli |
| 25 | 79.5 | 8.7 | 98 | US-09-249-471-21 | Sequence 21, Appli |
| 26 | 79.5 | 8.7 | 98 | US-09-249-471-21 | Sequence 21, Appli |
| 27 | 79.5 | 8.7 | 98 | US-08-809-455-21 | Sequence 21, Appli |

| | | | | | | |
|----|------|-----|-----|---|-------------------|--------------------|
| 28 | 79.5 | 8.7 | 98 | 3 | US-09-249-461-21 | Sequence 21, Appli |
| 29 | 79.5 | 8.7 | 98 | 3 | US-09-249-448-21 | Sequence 21, Appli |
| 30 | 78 | 8.6 | 518 | 1 | US-08-385-229-4 | Sequence 4, Appli |
| 31 | 77.5 | 8.5 | 75 | 2 | US-08-465-380-6 | Sequence 6, Appli |
| 32 | 77.5 | 8.5 | 75 | 2 | US-08-465-380-6 | Sequence 6, Appli |
| 33 | 77.5 | 8.5 | 75 | 2 | US-08-480-478-35 | Sequence 35, Appli |
| 34 | 77.5 | 8.5 | 75 | 2 | US-08-486-397-6 | Sequence 6, Appli |
| 35 | 77.5 | 8.5 | 75 | 2 | US-08-486-397-6 | Sequence 6, Appli |
| 36 | 77.5 | 8.5 | 75 | 2 | US-08-486-399-6 | Sequence 6, Appli |
| 37 | 77.5 | 8.5 | 75 | 2 | US-08-486-399-6 | Sequence 6, Appli |
| 38 | 77.5 | 8.5 | 75 | 2 | US-08-461-965-6 | Sequence 6, Appli |
| 39 | 77.5 | 8.5 | 75 | 2 | US-08-461-965-6 | Sequence 6, Appli |
| 40 | 77.5 | 8.5 | 75 | 2 | US-08-326-110A-35 | Sequence 35, Appli |
| 41 | 77.5 | 8.5 | 75 | 2 | US-08-634-641-6 | Sequence 6, Appli |
| 42 | 77.5 | 8.5 | 75 | 2 | US-08-634-641-6 | Sequence 6, Appli |
| 43 | 77.5 | 8.5 | 75 | 3 | US-09-249-471-6 | Sequence 6, Appli |
| 44 | 77.5 | 8.5 | 75 | 3 | US-09-249-471-6 | Sequence 6, Appli |
| 45 | 77.5 | 8.5 | 75 | 3 | US-09-249-472-6 | Sequence 6, Appli |

ALIGNMENTS

RESULT 1
US-08-810-572A-6
; Sequence 6, Application US/08810572A
; Patent No. 5969102
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,572A
FILING DATE: 28-FEB-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-810-572A-6
Query Match 100.0%; Score 909; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-90;

Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLSRRGSRGSRVDOERFPQGLMTGVAMRSCPEEQYMDPLGTGMSCKTICNHQSQR 60
DB 1 MSGLSRRGSRGSRVDOERFPQGLMTGVAMRSCPEEQYMDPLGTGMSCKTICNHQSQR 60

QY 61 TCAAFGRSLSCRKQKGFYDHLRDCISGASICGHPKQCAVFCENKLRSPVNLPEELRR 120
DB 61 TCAAFGRSLSCRKQKGFYDHLRDCISGASICGHPKQCAVFCENKLRSPVNLPEELRR 120

QY 121 QRSGEVENNSDNGRYQGLERHGRSEASPALPGLKLSADQVALVYST 166
DB 121 QRSGEVENNSDNGRYQGLERHGRSEASPALPGLKLSADQVALVYST 166

RESULT 2
US-09-290-333-6
Sequence 6, Application US/09290333
Patent No. 6316222
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/290,333
FILING DATE: 12-Apr-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-290-333-6

Query Match 100.0%; Score 909; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-90;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLSRRGSRGSRVDOERFPQGLMTGVAMRSCPEEQYMDPLGTGMSCKTICNHQSQR 60
DB 1 MSGLSRRGSRGSRVDOERFPQGLMTGVAMRSCPEEQYMDPLGTGMSCKTICNHQSQR 60

QY 61 TCAAFGRSLSCRKQKGFYDHLRDCISGASICGHPKQCAVFCENKLRSPVNLPEELRR 120

DB 61 TCAAFGRSLSCRKQKGFYDHLRDCISGASICGHPKQCAVFCENKLRSPVNLPEELRR 120

QY 121 QRSGEVENNSDNGRYQGLERHGRSEASPALPGLKLSADQVALVYST 166
DB 121 QRSGEVENNSDNGRYQGLERHGRSEASPALPGLKLSADQVALVYST 166

RESULT 3
US-08-810-572A-2
Sequence 2, Application US/08810572A
Patent No. 5969102
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,572A
FILING DATE: 28-FEB-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-810-572A-2

Query Match 100.0%; Score 909; DB 2; Length 293;
Best Local Similarity 100.0%; Pred. No. 4e-90;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLSRRGSRGSRVDOERFPQGLMTGVAMRSCPEEQYMDPLGTGMSCKTICNHQSQR 60
DB 1 MSGLSRRGSRGSRVDOERFPQGLMTGVAMRSCPEEQYMDPLGTGMSCKTICNHQSQR 60

QY 61 TCAAFGRSLSCRKQKGFYDHLRDCISGASICGHPKQCAVFCENKLRSPVNLPEELRR 120
DB 61 TCAAFGRSLSCRKQKGFYDHLRDCISGASICGHPKQCAVFCENKLRSPVNLPEELRR 120

QY 121 QRSGEVENNSDNGRYQGLERHGRSEASPALPGLKLSADQVALVYST 166
DB 121 QRSGEVENNSDNGRYQGLERHGRSEASPALPGLKLSADQVALVYST 166

RESULT 4
US-09-290-333-2
Sequence 2, Application US/09290333
Patent No. 6316222
GENERAL INFORMATION:
APPLICANT: Bratt, Richard J.
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 12-Apr-1999
APPLICATION NUMBER: US/09/290,333
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-290-333-2
Query Match
Best Local Similarity 100.0%; Score 909; DB 4; Length 293;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGIGSRGRGRSRVDOERPPQGLMTGVAMRSCPEEQYMDPLGTGNSCKTICNHQSOR 60
DB 1 MSGIGSRGRGRSRVDOERPPQGLMTGVAMRSCPEEQYMDPLGTGNSCKTICNHQSOR 60
QY 61 TCAPFCRSLCRKCKGKYDHLRPTCSASTCGHPKQCAFECNKRSPNLPPELR 120
DB 61 TCAPFCRSLCRKCKGKYDHLRPTCSASTCGHPKQCAFECNKRSPNLPPELR 120
QY 121 QRSGEVENNSDNGSGRYQGLERHGSASPALPGLKLSADQVALVYST 166
DB 121 QRSGEVENNSDNGSGRYQGLERHGSASPALPGLKLSADQVALVYST 166

RESULT 5
US-08-525-940-23
Sequence 23, Application US/08525940
Patent No. 5866351
GENERAL INFORMATION:
APPLICANT: Franzusoff, Alex
APPLICANT: Miranda, Luis R.

APPLICANT: Wolf, Joseph R.
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES AND GENES
TITLE OF INVENTION: ENCODING SAID PROTEASES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 07-JUL-1993
APPLICATION NUMBER: US 08/088,322
PRIOR APPLICATION DATA:
FILING DATE: 01-JAN-1995
APPLICATION NUMBER: US 08/368,852
FILING DATE: 07-JUL-1993
APPLICATION NUMBER: US 08/088,322
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-525-940-23
Query Match
Best Local Similarity 9.1%; Score 82.5; DB 2; Length 799;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;

QY 27 TGVAMRSCPEEQYMDPLGTGNSCKTICNHQSORTCAPF-----CR-----SLSC 71
DB 603 TNSCVTHCPDGSYDPTKKNLCRKCSENC-----XTCTEFHNCTECRDGLSLQSGRCSVSC 657
QY 72 RKEQKFFYDHLRPTCSASTC-----GHPKQC-----AYPCEN 106
DB 658 --EDGRYFNG--QDQPCHRRCATCAGAGADGCTNCTEGTFMED 657

RESULT 6
US-08-976-838-23
Sequence 23, Application US/08976838
Patent No. 5981259
GENERAL INFORMATION:
APPLICANT: Franzusoff, Alex
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASE NUCLEIC ACID
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,838
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-976-838-23

Query Match 9.1%; Score 82.5; DB 2; Length 799;
Best Local Similarity 26.0%; Pred. No. 1.5;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;

Qy 27 TGVAMRSCPEEQYMDPLGTCTCNHQSQTCAAF-----CR-----SLSC 71
Db 603 TNSCVTHCPDGSYQDTKXNLCKKCSENC-----KTCTEFHNCTEGRDGLSLQSRCSVSC 657
Qy 72 RKEQGFYDHLRLDCTICASCIC---GQHPKQC---AYFCEN 106
Db 658 --EDGRYFNG--QDCQPCHRFCATCAGAGADGCINCTEGYFME 697

RESULT 7

US-08-525-940-21
Sequence 21, Application US/08525940
Patent No. 5866351
GENERAL INFORMATION:
APPLICANT: Franzusoff, Alex
APPLICANT: Miranda, Luis R.
APPLICANT: Wolf, Joseph R.
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES AND GENES
TITLE OF INVENTION: ENCODING SAID PROTEASES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSES: Sheridan Rose & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,940
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/368,852
FILING DATE: 01-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/088,322
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700

TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 881 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-525-940-21

Query Match 9.1%; Score 82.5; DB 2; Length 881;
Best Local Similarity 26.0%; Pred. No. 1.7;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;

Qy 27 TGVAMRSCPEEQYMDPLGTCTCNHQSQTCAAF-----CR-----SLSC 71
Db 685 TNSCVTHCPDGSYQDTKXNLCKKCSENC-----KTCTEFHNCTEGRDGLSLQSRCSVSC 739
Qy 72 RKEQGFYDHLRLDCTICASCIC---GQHPKQC---AYFCEN 106
Db 740 --EDGRYFNG--QDCQPCHRFCATCAGAGADGCINCTEGYFME 779

RESULT 8

US-08-976-838-21
Sequence 21, Application US/08976838
Patent No. 5981259
GENERAL INFORMATION:
APPLICANT: Franzusoff, Alex
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASE NUCLEIC ACID
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSES: Sheridan Rose P.C.
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,838
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 881 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-976-838-21

Query Match 9.1%; Score 82.5; DB 2; Length 881;
Best Local Similarity 26.0%; Pred. No. 1.7;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;

Qy 27 TGVAMRSCPEEQYMDPLGTCTCNHQSQTCAAF-----CR-----SLSC 71
Db 685 TNSCVTHCPDGSYQDTKXNLCKKCSENC-----KTCTEFHNCTEGRDGLSLQSRCSVSC 739
Qy 72 RKEQGFYDHLRLDCTICASCIC---GQHPKQC---AYFCEN 106
Db 740 --EDGRYFNG--QDCQPCHRFCATCAGAGADGCINCTEGYFME 779

RESULT 9
US-08-525-940-18
Sequence 18, Application US/08525940
Patent No. 5866351
GENERAL INFORMATION:
APPLICANT: Franzsoeff, Alex
APPLICANT: Miranda, Luis R.
APPLICANT: Wolf, Joseph R.
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES AND GENES
TITLE OF INVENTION: ENCODING SAID PROTEASES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
City: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,940
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/368,852
FILING DATE: 01 JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/088,322
FILING DATE: 07 JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 915 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-525-940-18
Query Match 9.1%; Score 82.5; DB 2; Length 915;
Best Local Similarity 26.0%; Pred. No. 1.8;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;
QY 27 TGVAMRSCPEEQYNDPLIGTMSCKTICNHOSORTCAAF-----CR-----SLSC 71
DB 719 TNSCVTHCPDGSYDPTKKNLCRKCSENC-----KTCTEFHNCTEGRDGLSLQGSRCVSVC 773
QY 72 RKEQGKFDHLRDLICASCATC-----GQHPKQC-----AYPCEN 106
DB 774 --EDGRYFNG--QDCQPCRFATCAGAGADGCTNCTEGTYMED 813
RESULT 10
US-08-976-838-18
Sequence 18, Application US/08976838
Patent No. 5981259
GENERAL INFORMATION:
APPLICANT: Franzsoeff, Alex
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASE NUCLEIC ACID
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:

ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
City: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,838
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 915 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-976-838-18
Query Match 9.1%; Score 82.5; DB 2; Length 915;
Best Local Similarity 26.0%; Pred. No. 1.8;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;
QY 27 TGVAMRSCPEEQYNDPLIGTMSCKTICNHOSORTCAAF-----CR-----SLSC 71
DB 719 TNSCVTHCPDGSYDPTKKNLCRKCSENC-----KTCTEFHNCTEGRDGLSLQGSRCVSVC 773
QY 72 RKEQGKFDHLRDLICASCATC-----GQHPKQC-----AYPCEN 106
DB 774 --EDGRYFNG--QDCQPCRFATCAGAGADGCTNCTEGTYMED 813
RESULT 11
US-09-214-555B-2
Sequence 2, Application US/09214555B
Patent No. 6380171
GENERAL INFORMATION:
APPLICANT: INSTITUT DE RECHERCHE CLINIQUE DE MONTREAL
TITLE OF INVENTION: PRO-PROTEIN CONVERTING ENZYME
FILE REFERENCE: PRO-PROTEIN CONVERTING ENZ
CURRENT APPLICATION NUMBER: US/09/214,555B
PRIOR FILING DATE: 1999-01-04
PRIOR APPLICATION NUMBER: 60/021,008
PRIOR FILING DATE: 1996-07-26
PRIOR APPLICATION NUMBER: 2,203,745
PRIOR FILING DATE: 1997-04-25
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 2
LENGTH: 915
TYPE: PRT
ORGANISM: Homo sapiens
US-09-214-555B-2
Query Match 9.1%; Score 82.5; DB 4; Length 915;
Best Local Similarity 26.0%; Pred. No. 1.8;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;
QY 27 TGVAMRSCPEEQYNDPLIGTMSCKTICNHOSORTCAAF-----CR-----SLSC 71
DB 719 TNSCVTHCPDGSYDPTKKNLCRKCSENC-----KTCTEFHNCTEGRDGLSLQGSRCVSVC 773

Oy 72 RKEGKFYDHLRLDCLSCASIC-----GQHPKOC-----AYFCEN 106
Db 774 --EDGRYFNG--QDCOPCHRFATCAGAGADGACINCTEGYFMD 813

RESULT 12

US-09-214-555B-7
; Sequence 7, Application US/09214555B
; Patent No. 6380171
; GENERAL INFORMATION:
; APPLICANT: INSTITUT DE RECHERCHE CLINIQUE DE MONTREAL
; TITLE OF INVENTION: PRO-PROTEIN CONVERTING ENZYME
; FILE REFERENCE: PRO-PROTEIN CONVERT ENZ
; CURRENT APPLICATION NUMBER: US/09/214,555B
; PRIOR FILING DATE: 1999-01-04
; PRIOR APPLICATION NUMBER: 60/021,008
; PRIOR FILING DATE: 1996-07-26
; PRIOR APPLICATION NUMBER: 2,203,745
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-214-555B-7

Query Match 9.1%; Score 82.5; DB 4; Length 915;
Best Local Similarity 26.0%; Pred. No. 1.8;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;

Oy 27 TGVAMRSCPEEQYWDPLGTCMSCKTICNHQSORTCAAF-----CR-----SLSC 71
Db 719 TNSCVTHCPDGSYQPTKMLCRKSENC-----KTCTEFHNTCTEBCRDGLSLGSRCSVSC 773
Oy 72 RKEGKFYDHLRLDCLSCASIC-----GQHPKOC-----AYFCEN 106
Db 774 --EDGRYFNG--QDCOPCHRFATCAGAGADGACINCTEGYFMD 813

RESULT 13

US-09-590-656-2
; Sequence 2, Application US/09590656
; Patent No. 6413932
; GENERAL INFORMATION:
; APPLICANT: Cerretti, Douglas P.
; APPLICANT: Borges, Luis G.
; APPLICANT: Fanlow, III, William C.
; TITLE OF INVENTION: TEK ANTAGONISTS
; FILE REFERENCE: 2900-A
; CURRENT APPLICATION NUMBER: US/09/590,656
; CURRENT FILING DATE: 2000-06-07
; PRIOR APPLICATION NUMBER: 60/137,889
; PRIOR FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 704
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-590-656-2

Query Match 8.9%; Score 81; DB 4; Length 704;
Best Local Similarity 24.2%; Pred. No. 1.8;
Matches 39; Conservative 15; Mismatches 63; Indels 44; Gaps 8;

Oy 26 WTGVAMRSCPEEQYWDPLGTCM-----SCKTICN-HSQ 59
Db 203 FTFLIVRRC-EAQKMGPCPNHLCCTACMNNVCHBDTGCICPPGFMGRTCERACELHTFG 261
Oy 60 RTCAAFCSLSRKEGKFYDHLRLDCLSCASICGQHPKOCAYFCENKLRSPVNLPELR 119
Db 262 RTCKERCSG---QEGCKSYFCLPDPYGCSCATGWKGLQCNEACH-----FGFYGPDC 312

Oy 120 RQRSGEVNNSDNGRYQGLEHRSSEASPALGLKLSADQV 160
Db 313 LRCSC---NNGEMCDRFQ-----GCLCSFGWQGLQCEREGI 345

RESULT 14

US-09-590-656-1
; Sequence 1, Application US/09590656
; Patent No. 6413932
; GENERAL INFORMATION:
; APPLICANT: Cerretti, Douglas P.
; APPLICANT: Borges, Luis G.
; APPLICANT: Fanlow, III, William C.
; TITLE OF INVENTION: TEK ANTAGONISTS
; FILE REFERENCE: 2900-A
; CURRENT APPLICATION NUMBER: US/09/590,656
; CURRENT FILING DATE: 2000-06-07
; PRIOR APPLICATION NUMBER: 60/137,889
; PRIOR FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-590-656-1

Query Match 8.9%; Score 81; DB 4; Length 977;
Best Local Similarity 24.2%; Pred. No. 2.8;
Matches 39; Conservative 15; Mismatches 63; Indels 44; Gaps 8;

Oy 26 WTGVAMRSCPEEQYWDPLGTCM-----SCKTICN-HSQ 59
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Oy 60 RTCAAFCSLSRKEGKFYDHLRLDCLSCASICGQHPKOCAYFCENKLRSPVNLPELR 119
Db 262 RTCKERCSG---QEGCKSYFCLPDPYGCSCATGWKGLQCNEACH-----FGFYGPDC 312
Oy 120 RQRSGEVNNSDNGRYQGLEHRSSEASPALGLKLSADQV 160
Db 313 LRCSC---NNGEMCDRFQ-----GCLCSFGWQGLQCEREGI 345

RESULT 15

US-08-323-474-2
; Sequence 2, Application US/08323474
; Patent No. 5447860
; GENERAL INFORMATION:
; APPLICANT: Ziegler, Steven F.
; TITLE OF INVENTION: NOVEL TYROSINE KINASE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,474
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/905,600
; FILING DATE: 26-JUN-1992
; ATTORNEY/AGENT INFORMATION:

NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2609
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-323-474-2

Query Match 8.9%; Score 81; DB 1; Length 1124;
Best Local Similarity 24.2%; Pred. No. 3.3;
Matches 39; Conservative 15; Mismatches 63; Indels 44; Gaps 8;

Qy 26 WTGVAMRSCPEEOYWDP-----LLGTGM-----SKTICM-HQSQ 59
Db 203 FTRLIVRRC-EAQMGPBCNHLCTACMANGVCHEDTGEICIPPGFMGRCTEKACGLHTFG 261
Qy 60 RTCAAFCRSLSCRIEKGKFDYHLIRDCISASICGHPKQCAVFCENKLRSPVNLPELR 119
Db 262 RTCKERCSSG---QEGCKSYVFCLPDPYGCSCATGWMKGLQCNEACH-----FGFYGPDCX 312
Qy 120 RQSGVEVNNSDNGRYQGLHRGSEASPALPGLKLSADQV 160
Db 313 LRCSG---NNGEMQDRFQ-----GCLCSFGWQGLQCEREGET 345

Search completed: February 4, 2003, 13:00:17
Job time: 17.4575 secs

GenCore version 5.1.3
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OM protein - protein search, using SW model

Run on: February 4, 2003, 12:59:16 ; Search time 10.753 Seconds
(without alignments)
342.239 Million cell updates/sec

Title: US-09-854-864-15
Perfect score: 909
Sequence: 1 MSGIGSRGRGRSRVDGEER.....SPALPGIKLSADQVALVYST 166

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Gapop 10.0 , Gapext 0.5

Searched: 129505 seqs, 22169297 residues

Total number of hits satisfying chosen parameters: 129505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications MA:*

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------------------|-------------------|
| 1 | 909 | 100.0 | 166 | 10 US-09-854-864-15 | Sequence 15, Appl |
| 2 | 909 | 100.0 | 293 | 9 US-09-779-050A-42 | Sequence 42, Appl |
| 3 | 909 | 100.0 | 293 | 9 US-10-084-971-2 | Sequence 2, Appl |
| 4 | 909 | 100.0 | 293 | 9 US-10-068-725-4 | Sequence 4, Appl |
| 5 | 909 | 100.0 | 293 | 9 US-09-302-863-2 | Sequence 2, Appl |
| 6 | 909 | 100.0 | 293 | 10 US-09-879-919-22 | Sequence 12, Appl |
| 7 | 909 | 100.0 | 293 | 10 US-09-854-864-14 | Sequence 14, Appl |
| 8 | 909 | 100.0 | 293 | 10 US-09-961-376-2 | Sequence 2, Appl |
| 9 | 904 | 99.4 | 397 | 10 US-09-854-864-18 | Sequence 18, Appl |
| 10 | 894.5 | 98.4 | 291 | 9 US-09-779-050A-43 | Sequence 43, Appl |
| 11 | 393 | 43.2 | 67 | 10 US-09-854-864-16 | Sequence 16, Appl |
| 12 | 342 | 37.6 | 59 | 10 US-09-854-864-20 | Sequence 20, Appl |
| 13 | 279.5 | 30.7 | 57 | 9 US-09-779-050A-47 | Sequence 47, Appl |
| 14 | 224 | 24.6 | 38 | 9 US-09-779-050A-46 | Sequence 46, Appl |
| 15 | 218 | 24.0 | 37 | 9 US-09-779-050A-45 | Sequence 45, Appl |
| 16 | 168 | 18.5 | 32 | 9 US-09-779-050A-44 | Sequence 44, Appl |
| 17 | 93 | 10.2 | 81 | 10 US-09-854-864-13 | Sequence 13, Appl |
| 18 | 87.5 | 9.6 | 463 | 9 US-09-905-291A-285 | Sequence 285, App |
| 19 | 87.5 | 9.6 | 463 | 9 US-09-902-853-285 | Sequence 285, App |

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|----|------|-----|------|-----------------------|-------------------|
| 20 | 87.5 | 9.6 | 463 | 9 US-09-907-824-285 | Sequence 285, App |
| 21 | 87.5 | 9.6 | 463 | 9 US-09-907-841-285 | Sequence 285, App |
| 22 | 87.5 | 9.6 | 463 | 9 US-09-904-011-285 | Sequence 285, App |
| 23 | 87.5 | 9.6 | 463 | 9 US-10-028-072-360 | Sequence 360, App |
| 24 | 87.5 | 9.6 | 463 | 9 US-09-906-742-285 | Sequence 285, App |
| 25 | 87.5 | 9.6 | 463 | 9 US-10-121-049-360 | Sequence 360, App |
| 26 | 87.5 | 9.6 | 463 | 9 US-10-123-904-360 | Sequence 360, App |
| 27 | 87.5 | 9.6 | 463 | 9 US-10-140-470-360 | Sequence 360, App |
| 28 | 87.5 | 9.6 | 463 | 10 US-09-909-320-285 | Sequence 285, App |
| 29 | 87.5 | 9.6 | 463 | 10 US-09-909-088B-285 | Sequence 285, App |
| 30 | 87 | 9.6 | 207 | 9 US-10-077-438-3 | Sequence 3, Appl |
| 31 | 87 | 9.6 | 207 | 9 US-10-077-137-3 | Sequence 3, Appl |
| 32 | 87 | 9.6 | 292 | 10 US-09-745-763-166 | Sequence 166, App |
| 33 | 86 | 9.5 | 231 | 10 US-09-840-795-19 | Sequence 19, Appl |
| 34 | 86 | 9.5 | 229 | 9 US-10-119-466-12 | Sequence 12, Appl |
| 35 | 84 | 9.2 | 77 | 10 US-09-840-795-17 | Sequence 17, Appl |
| 36 | 82.5 | 9.1 | 225 | 9 US-10-185-770-4 | Sequence 4, Appl |
| 37 | 81 | 8.9 | 586 | 9 US-10-092-390-4 | Sequence 4, Appl |
| 38 | 81 | 8.9 | 1140 | 9 US-10-092-390-2 | Sequence 2, Appl |
| 39 | 79.5 | 8.7 | 1172 | 9 US-09-974-298-56 | Sequence 56, Appl |
| 40 | 79.5 | 8.7 | 1172 | 10 US-09-919-172-16 | Sequence 16, Appl |
| 41 | 78.5 | 8.6 | 399 | 10 US-09-907-372-1 | Sequence 1, Appl |
| 42 | 77.5 | 8.5 | 220 | 9 US-10-042-141-54 | Sequence 54, Appl |
| 43 | 77.5 | 8.5 | 220 | 10 US-09-726-643-54 | Sequence 54, Appl |
| 44 | 77.5 | 8.5 | 514 | 10 US-09-800-729-124 | Sequence 124, App |
| 45 | 77.5 | 8.5 | 1745 | 10 US-09-800-729-89 | Sequence 89, Appl |

ALIGNMENTS

RESULT 1

US-09-854-864-15
Sequence 15, Application US/09854864
Patent No. US20020081296A1
GENERAL INFORMATION: THIELL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLVS/ACP-3, AND TACI
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 166
TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-864-15

Query Match 100.0%; Score 909; DB 10; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.5e-75;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGIGSRGRGRSRVDGEERPPQGLMTGVAMRSCPEEQYMDPLLTGCMSCKTTICNHQSR 60
DB 1 MSGIGSRGRGRSRVDGEERPPQGLMTGVAMRSCPEEQYMDPLLTGCMSCKTTICNHQSR 60
QY 61 TCAACRBLSCRKQKGYDHLRDCISCAICGHPQCAVFCENKLRSPVNLPELR 120
DB 61 TCAACRBLSCRKQKGYDHLRDCISCAICGHPQCAVFCENKLRSPVNLPELR 120
QY 121 QRSGEVNNSDNSGRYQGLERHGESEAPALPGIKLSADQVALVYST 166
DB 121 QRSGEVNNSDNSGRYQGLERHGESEAPALPGIKLSADQVALVYST 166
RESULT 2

US-09-779-050A-42
; Sequence 42, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-42

Query Match 100.0%; Score 909; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.8e-75;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MSGGSRGRGSRVDOERFPQGLMTGVAMRSCPEEQYWDPLGTGMSCKTICNHQSQR 60
Qy 61 TCAAFCSRSLSCRKEQGFYDHLRDCISCAICGQHPKQCAVFCENKLRSPVNLPEELRR 120
Db 61 TCAAFCSRSLSCRKEQGFYDHLRDCISCAICGQHPKQCAVFCENKLRSPVNLPEELRR 120
Qy 121 QRSGEVNNSDNSGRYQGLERHGESEASPALPGLKLSADQVALVYST 166
Db 121 QRSGEVNNSDNSGRYQGLERHGESEASPALPGLKLSADQVALVYST 166

RESULT 3
US-10-084-971-2
; Sequence 2, Application US/10084971
; Publication No. US20020187526A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Neutrokin- α Binding Proteins and Methods Based Thereon
; FILE REFERENCE: PFS24PCT
; CURRENT APPLICATION NUMBER: US/10/084,971
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/533,822
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/126,599
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/188,208
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-084-971-2

Query Match 100.0%; Score 909; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.8e-75;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 TCAAFCSRSLSCRKEQGFYDHLRDCISCAICGQHPKQCAVFCENKLRSPVNLPEELRR 120
Db 61 TCAAFCSRSLSCRKEQGFYDHLRDCISCAICGQHPKQCAVFCENKLRSPVNLPEELRR 120

Qy 121 QRSGEVNNSDNSGRYQGLERHGESEASPALPGLKLSADQVALVYST 166
Db 121 QRSGEVNNSDNSGRYQGLERHGESEASPALPGLKLSADQVALVYST 166

RESULT 4
US-10-068-725-4
; Sequence 4, Application US/10068725
; Publication No. US20030012783A1
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne
; TITLE OF INVENTION: Antibodies That Bind Both BCMA and TACI
; FILE REFERENCE: 01-04
; CURRENT APPLICATION NUMBER: US/10/068,725
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/270,274
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/283,447
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-725-4

Query Match 100.0%; Score 909; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.8e-75;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MSGGSRGRGSRVDOERFPQGLMTGVAMRSCPEEQYWDPLGTGMSCKTICNHQSQR 60
Qy 61 TCAAFCSRSLSCRKEQGFYDHLRDCISCAICGQHPKQCAVFCENKLRSPVNLPEELRR 120
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Qy 121 QRSGEVNNSDNSGRYQGLERHGESEASPALPGLKLSADQVALVYST 166
Db 121 QRSGEVNNSDNSGRYQGLERHGESEASPALPGLKLSADQVALVYST 166

RESULT 5
US-09-302-863-2
; Sequence 2, Application US/09302863
; Publication No. US20030022233A1
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G
; APPLICANT: Din, Manwan S.
; TITLE OF INVENTION: METHODS OF USE OF THE TACI/TACI-L INTERACTION
; FILE REFERENCE: 2519
; CURRENT APPLICATION NUMBER: US/09/302,863
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Human
US-09-302-863-2

Query Match 100.0%; Score 909; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.8e-75;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSGGSRGRGSRVDOERFPQGLMTGVAMRSCPEEQYWDPLGTGMSCKTICNHQSQR 60
Db 1 MSGGSRGRGSRVDOERFPQGLMTGVAMRSCPEEQYWDPLGTGMSCKTICNHQSQR 60
Qy 61 TCAAFCSRSLSCRKEQGFYDHLRDCISCAICGQHPKQCAVFCENKLRSPVNLPEELRR 120
Db 61 TCAAFCSRSLSCRKEQGFYDHLRDCISCAICGQHPKQCAVFCENKLRSPVNLPEELRR 120

Db 61 TCAACRSLSCRKEQGYDHLRLDLCISGCHPQKCAVFCENKLRSPVNLPELRR 120
 QY 121 ORSGEVNNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVYST 166
 Db 121 ORSGEVNNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVYST 166

RESULT 6

US-09-879-919-22
 ; Sequence 22, Application US/09879919
 ; Patent No. US20020064829A1
 ; GENERAL INFORMATION:

APPLICANT: Yu, Guo-Liang, et al.

TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
 FILE REFERENCE: PF25321

CURRENT APPLICATION NUMBER: US/09/879,919

CURRENT FILING DATE: 2001-06-14

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/277,978

PRIOR FILING DATE: 2001-03-23

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/254,875

PRIOR FILING DATE: 2000-12-13

PRIOR APPLICATION NUMBER: 60/241,952

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/211,537

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 08/815,783

PRIOR FILING DATE: 1997-03-12

PRIOR APPLICATION NUMBER: 60/016,812

PRIOR FILING DATE: 1996-03-14

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 22

LENGTH: 293

TYPE: PRT

ORGANISM: Homo sapiens

US-09-879-919-22

Query Match

Best Local Similarity 100.0%; Score 909; DB 10; Length 293;

Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLSRRGGRSVYDOERFPQGLMTGVAMRSCPEBOYMDPLGTGMSCKTICNHQSOR 60

Db 1 MSGLSRRGGRSVYDOERFPQGLMTGVAMRSCPEBOYMDPLGTGMSCKTICNHQSOR 60

QY 61 TCAACRSLSCRKEQGYDHLRLDLCISGCHPQKCAVFCENKLRSPVNLPELRR 120

Db 61 TCAACRSLSCRKEQGYDHLRLDLCISGCHPQKCAVFCENKLRSPVNLPELRR 120

QY 121 ORSGEVNNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVYST 166

Db 121 ORSGEVNNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVYST 166

RESULT 7

US-09-854-864-14

; Sequence 14, Application US/09854864

; Patent No. US20020081296A1

; GENERAL INFORMATION:

APPLICANT: XU, GANG

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

FILE REFERENCE: A-684B

CURRENT APPLICATION NUMBER: US/09/854,864

CURRENT FILING DATE: 2001-09-11

PRIOR APPLICATION NUMBER: US 60/204,039

PRIOR FILING DATE: 2000-05-12

PRIOR APPLICATION NUMBER: US 60/214,591

; PRIOR FILING DATE: 2000-06-27
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 14
 ; LENGTH: 293
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-854-864-14

Query Match 100.0%; Score 909; DB 10; Length 293;
 Best Local Similarity 100.0%; Pred. No. 2.8e-75;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLSRRGGRSVYDOERFPQGLMTGVAMRSCPEBOYMDPLGTGMSCKTICNHQSOR 60

Db 1 MSGLSRRGGRSVYDOERFPQGLMTGVAMRSCPEBOYMDPLGTGMSCKTICNHQSOR 60

QY 61 TCAACRSLSCRKEQGYDHLRLDLCISGCHPQKCAVFCENKLRSPVNLPELRR 120

Db 61 TCAACRSLSCRKEQGYDHLRLDLCISGCHPQKCAVFCENKLRSPVNLPELRR 120

QY 121 ORSGEVNNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVYST 166

Db 121 ORSGEVNNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVYST 166

RESULT 8

US-09-961-376-2

; Sequence 2, Application US/09961376

; Patent No. US20020106736A1

; GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR17

FILE REFERENCE: PF524P1

CURRENT APPLICATION NUMBER: US/09/961,376

CURRENT FILING DATE: 2001-09-25

PRIOR APPLICATION NUMBER: 60/254,874

PRIOR FILING DATE: 2000-12-13

PRIOR APPLICATION NUMBER: 60/235,991

PRIOR FILING DATE: 2000-09-26

PRIOR APPLICATION NUMBER: 09/533,822

PRIOR FILING DATE: 2000-03-24

PRIOR APPLICATION NUMBER: 60/188,208

PRIOR FILING DATE: 2000-03-10

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 293

TYPE: PRT

ORGANISM: Homo sapiens

US-09-961-376-2

Query Match

Best Local Similarity 100.0%; Score 909; DB 10; Length 293;

Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLSRRGGRSVYDOERFPQGLMTGVAMRSCPEBOYMDPLGTGMSCKTICNHQSOR 60

Db 1 MSGLSRRGGRSVYDOERFPQGLMTGVAMRSCPEBOYMDPLGTGMSCKTICNHQSOR 60

QY 61 TCAACRSLSCRKEQGYDHLRLDLCISGCHPQKCAVFCENKLRSPVNLPELRR 120

Db 61 TCAACRSLSCRKEQGYDHLRLDLCISGCHPQKCAVFCENKLRSPVNLPELRR 120

QY 121 ORSGEVNNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVYST 166

Db 121 ORSGEVNNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVYST 166

RESULT 9

US-09-854-864-18

; Sequence 18, Application US/09854864

; Patent No. US20020081296A1

```
/ GENERAL INFORMATION:
/ APPLICANT: THEILL, LARS EYDE
/ APPLICANT: YU, GANG
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
/ FILE REFERENCE: A-686B
/ CURRENT APPLICATION NUMBER: US/09/854,864
/ CURRENT FILING DATE: 2001-09-11
/ PRIOR APPLICATION NUMBER: US 60/204,039
/ PRIOR FILING DATE: 2000-05-12
/ PRIOR APPLICATION NUMBER: US 60/214,591
/ PRIOR FILING DATE: 2000-06-27
/ NUMBER OF SEQ ID NOS: 31
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 18
/ LENGTH: 397
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-854-864-18
```

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Query Match          99.4%; Score 904; DB 10; Length 397;
Best Local Similarity 100.0%; Pred. No. 1.1e-74;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MSGLGRSRGRGSRVDQERFPGGLTGVAMRSCPEEQYWDPLGTGCMCKTICNHQSQR 60
DB 1 MSGLGRSRGRGSRVDQERFPGGLTGVAMRSCPEEQYWDPLGTGCMCKTICNHQSQR 60
QY 61 TCAAFCRSLSCRKEQKFDHLRDCISCAICGQHPKQCAVFCENKLSPVNLPPELRR 120
DB 61 TCAAFCRSLSCRKEQKFDHLRDCISCAICGQHPKQCAVFCENKLSPVNLPPELRR 120
QY 121 ORSGVEVNNSDNSGRYQGLEHRSSEASPALPGIKLSADQVALVYS 165
DB 121 ORSGVEVNNSDNSGRYQGLEHRSSEASPALPGIKLSADQVALVYS 165
```

```
RESULT 10
US-09-779-050A-43
/ Sequence 43, Application US/09779050A
/ Patent No. US20020160416A1
/ GENERAL INFORMATION:
/ APPLICANT: BOYLE, WILLIAM
/ APPLICANT: HSU, HAILING
/ TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
/ FILE REFERENCE: A-570B
/ CURRENT APPLICATION NUMBER: US/09/779,050A
/ CURRENT FILING DATE: 2001-02-12
/ PRIOR APPLICATION NUMBER: 60/181,800
/ PRIOR FILING DATE: 2000-02-11
/ NUMBER OF SEQ ID NOS: 52
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 43
/ LENGTH: 291
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-779-050A-43
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Query Match          98.4%; Score 894.5; DB 9; Length 291;
Best Local Similarity 99.4%; Pred. No. 5.7e-74;
Matches 165; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
```

```
QY 1 MSGLGRSRGRGSRVDQERFPGGLTGVAMRSCPEEQYWDPLGTGCMCKTICNHQSQR 60
DB 1 MSGLGRSRGRGSRVDQERFPGGLTGVAMRSCPEEQYWDPLGTGCMCKTICNHQSQR 60
QY 61 TCAAFCRSLSCRKEQKFDHLRDCISCAICGQHPKQCAVFCENKLSPVNLPPELRR 120
DB 61 TCAAFCRSLSCRKEQKFDHLRDCISCAICGQHPKQCAVFCENKLSPVNLPPELRR 120
QY 121 ORSGVEVNNSDNSGRYQGLEHRSSEASPALPGIKLSADQVALVYS 166
DB 121 ORSGVEVNNSDNSGRYQGLEHRSSEASPALPGIKLSADQVA-VYST 165
```

```
RESULT 11
US-09-854-864-16
/ Sequence 16, Application US/09854864
/ Patent No. US20020081296A1
/ GENERAL INFORMATION:
/ APPLICANT: THEILL, LARS EYDE
/ APPLICANT: YU, GANG
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
/ FILE REFERENCE: A-686B
/ CURRENT APPLICATION NUMBER: US/09/854,864
/ CURRENT FILING DATE: 2001-09-11
/ PRIOR APPLICATION NUMBER: US 60/204,039
/ PRIOR FILING DATE: 2000-05-12
/ PRIOR APPLICATION NUMBER: US 60/214,591
/ PRIOR FILING DATE: 2000-06-27
/ NUMBER OF SEQ ID NOS: 31
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 16
/ LENGTH: 67
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-854-864-16
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Query Match          43.2%; Score 393; DB 10; Length 67;
Best Local Similarity 94.4%; Pred. No. 3e-29;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
```

```
QY 34 CPEEQYWDPLGTGCMCKTICNHQSORTCAAFCRSLSCRKEQKFDHLRDCISCAIC 93
DB 1 CPEEQYWDPLGTGCMCKTICNHQSORTCAAFCRSLSCRKEQKFDHLRDCISCAIC 93
QY 94 GQHPKQCAVFC 104
DB 57 GQHPKQCAVFC 67
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```
RESULT 12
US-09-854-864-20
/ Sequence 20, Application US/09854864
/ Patent No. US20020081296A1
/ GENERAL INFORMATION:
/ APPLICANT: THEILL, LARS EYDE
/ APPLICANT: YU, GANG
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
/ FILE REFERENCE: A-686B
/ CURRENT APPLICATION NUMBER: US/09/854,864
/ CURRENT FILING DATE: 2001-09-11
/ PRIOR APPLICATION NUMBER: US 60/204,039
/ PRIOR FILING DATE: 2000-05-12
/ PRIOR APPLICATION NUMBER: US 60/214,591
/ PRIOR FILING DATE: 2000-06-27
/ NUMBER OF SEQ ID NOS: 31
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 20
/ LENGTH: 59
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-854-864-20
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Query Match          37.6%; Score 342; DB 10; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.1e-24;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 34 CPEEQYWDPLGTGCMCKTICNHQSORTCAAFCRSLSCRKEQKFDHLRDCISCAIC 92
DB 1 CPEEQYWDPLGTGCMCKTICNHQSORTCAAFCRSLSCRKEQKFDHLRDCISCAIC 92
```

```
RESULT 13
```


US-09-779-050A-47
 ; Sequence 47, Application US/0979050A
 ; Patent No. US20020160416A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BOYLE, WILLIAM
 ; APPLICANT: HSU, HAILING
 ; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
 ; FILE REFERENCE: A-570B
 ; CURRENT APPLICATION NUMBER: US/09/779,050A
 ; CURRENT FILING DATE: 2001-02-12
 ; PRIOR APPLICATION NUMBER: 60/181,800
 ; PRIOR FILING DATE: 2000-02-11
 ; NUMBER OF SEQ ID NOS: 52
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 47
 ; LENGTH: 57
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-779-050A-47

Query Match 30.7%; Score 279.5; DB 9; Length 57;
 Best Local Similarity 98.3%; Pred. No. 4.8e-19;
 Matches 57; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 108 LRSFVNLPEELRRDRSGEYNNNSDNGRYQGLEHRSSEASPALPGIKLSADQVALVYS 165
 Db 1 LRSFVNLPEELRRDRSGEYNNNSDNGRYQGLEHRSSEASPALPGIKLSADQVA-VYS 57

RESULT 14
 US-09-779-050A-46
 ; Sequence 46, Application US/09779050A
 ; Patent No. US20020160416A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BOYLE, WILLIAM
 ; APPLICANT: HSU, HAILING
 ; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
 ; FILE REFERENCE: A-570B
 ; CURRENT APPLICATION NUMBER: US/09/779,050A
 ; CURRENT FILING DATE: 2001-02-12
 ; PRIOR APPLICATION NUMBER: 60/181,800
 ; PRIOR FILING DATE: 2000-02-11
 ; NUMBER OF SEQ ID NOS: 52
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 46
 ; LENGTH: 38
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-779-050A-46

Query Match 24.6%; Score 224; DB 9; Length 38;
 Best Local Similarity 100.0%; Pred. No. 3.3e-14;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 SCRKEQGFYDHLIRDCISCAISICGQHPKQCAVFCENK 107
 Db 1 SCRKEQGFYDHLIRDCISCAISICGQHPKQCAVFCENK 38

RESULT 15
 US-09-779-050A-45
 ; Sequence 45, Application US/09779050A
 ; Patent No. US20020160416A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BOYLE, WILLIAM
 ; APPLICANT: HSU, HAILING
 ; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
 ; FILE REFERENCE: A-570B
 ; CURRENT APPLICATION NUMBER: US/09/779,050A
 ; CURRENT FILING DATE: 2001-02-12
 ; PRIOR APPLICATION NUMBER: 60/181,800
 ; PRIOR FILING DATE: 2000-02-11
 ; NUMBER OF SEQ ID NOS: 52

; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 45
 ; LENGTH: 37
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-779-050A-45

Query Match 24.0%; Score 218; DB 9; Length 37;
 Best Local Similarity 100.0%; Pred. No. 1.1e-13;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 SCPEQYWDPLIGTCMSCKTICNHSQRTCAAFCSL 69
 Db 1 SCPEQYWDPLIGTCMSCKTICNHSQRTCAAFCSL 37

Search completed: February 4, 2003, 13:05:58
 Job time : 11.753 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 4, 2003, 12:52:56 ; Search time 42.3401 Seconds
(without alignments) ;
522.427 Million cell updates/sec

Title: US-09-854-864-15

Perfect score: 1 MSGIGRSGRSGRSGRVDQEE.....SPALPGKLSADQVALVYST 166

Sequence: BLOSUM62

Scoring table: Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 909 | 100.0 | 166 | 19 | AAW5785 |
| 2 | 909 | 100.0 | 166 | 23 | AAE15494 |
| 3 | 909 | 100.0 | 265 | 22 | AAE09244 |
| 4 | 909 | 100.0 | 293 | 19 | AAW5783 |
| 5 | 909 | 100.0 | 293 | 21 | AAE15494 |
| 6 | 909 | 100.0 | 293 | 21 | AAE09240 |
| 7 | 909 | 100.0 | 293 | 22 | AAE09240 |
| 8 | 909 | 100.0 | 293 | 22 | AAE15494 |
| 9 | 909 | 100.0 | 293 | 23 | AAU95512 |
| 10 | 909 | 100.0 | 293 | 23 | AAE15494 |

| | | | | | | |
|----|-------|-------|------|----|----------|---------------------|
| 11 | 909 | 100.0 | 293 | 23 | AAO14130 | Human transmembran |
| 12 | 909 | 100.0 | 293 | 23 | AAU75408 | Tumour necrosis fa |
| 13 | 909 | 100.0 | 293 | 23 | AAE15493 | Human transmembran |
| 14 | 909 | 100.0 | 293 | 23 | AAU09900 | Human AGP-3 relat |
| 15 | 909 | 99.4 | 312 | 23 | AAO14135 | Protein of N-termi |
| 16 | 904 | 99.4 | 397 | 23 | AAE15498 | Human TRAC1-immunog |
| 17 | 894.5 | 98.4 | 291 | 23 | AAU10949 | Human AGP-3 recept |
| 18 | 881 | 96.9 | 404 | 23 | AAO14136 | Protein of a compl |
| 19 | 651 | 71.6 | 366 | 23 | AAO14132 | Protein of hTRAC1 (|
| 20 | 599 | 65.9 | 247 | 21 | AAE15498 | Human BR43x2, an i |
| 21 | 480.5 | 54.0 | 334 | 23 | AAO14133 | Protein of hTRAC1 (|
| 22 | 419.5 | 46.1 | 249 | 21 | AAE15498 | A murine znfn4, a |
| 23 | 342 | 37.6 | 59 | 23 | AAE15500 | Human TRAC1 cytein |
| 24 | 279.5 | 30.7 | 57 | 23 | AAU10953 | Human AGP-3 recept |
| 25 | 224 | 24.6 | 38 | 23 | AAU10952 | Human AGP-3 recept |
| 26 | 218 | 24.0 | 37 | 23 | AAU10951 | Human AGP-3 recept |
| 27 | 204 | 22.4 | 34 | 23 | AAE15496 | Human TRAC1 cytein |
| 28 | 201 | 22.1 | 33 | 23 | AAE15495 | Human TRAC1 cytein |
| 29 | 168 | 18.5 | 32 | 23 | AAU10950 | Human AGP-3 recept |
| 30 | 95 | 10.5 | 197 | 21 | AAE15491 | Human TRNGO 140-2. |
| 31 | 93 | 10.2 | 1589 | 22 | AAE15495 | Human polypeptide |
| 32 | 93 | 10.2 | 1727 | 22 | AAE15495 | Human polypeptide |
| 33 | 93 | 10.2 | 1878 | 22 | AAE15495 | Human polypeptide |
| 34 | 92 | 10.1 | 266 | 22 | AAE15495 | Human polypeptide |
| 35 | 89 | 9.8 | 1878 | 19 | AAE15495 | Human BAZ2-alpha p |
| 36 | 88.5 | 9.7 | 665 | 22 | AAE15495 | Drosophila melanog |
| 37 | 88 | 9.7 | 795 | 22 | AAE15495 | Novel human diagno |
| 38 | 87.5 | 9.6 | 463 | 20 | AAE15495 | Amino acid sequenc |
| 39 | 87.5 | 9.6 | 463 | 21 | AAE15495 | Neuron-associated |
| 40 | 87.5 | 9.6 | 463 | 21 | AAE15495 | Human PRO328 antit |
| 41 | 87.5 | 9.6 | 463 | 22 | AAE15495 | Human PRO328 polyp |
| 42 | 87.5 | 9.6 | 463 | 22 | AAE15495 | Human membrane or |
| 43 | 87.5 | 9.6 | 463 | 22 | AAE15495 | Human PRO328 prote |
| 44 | 87.5 | 9.6 | 463 | 22 | AAE15495 | Human angiogenesis |
| 45 | 87 | 9.6 | 251 | 22 | AAE15495 | Human mature stem |

ALIGNMENTS

| | | |
|----------|---|----------------------------|
| RESULT 1 | AAW5785 | standard; Protein; 166 AA. |
| XX | AAW5785; | |
| AC | AAW5785; | |
| XX | 18-JAN-1999 | (first entry) |
| DT | 18-JAN-1999 | |
| XX | Human lymphocyte surface receptor extracellular domain. | |
| XX | TACT1; transmembrane activator and CAML-interactor; | |
| XX | calcium signal-modulating cyclophilin ligand; human; | |
| XX | lymphocyte surface receptor; human; B-cell; B lymphocyte; | |
| XX | infection; cancer; rheumatoid arthritis; autoimmune disease; | |
| XX | glomerulonephritis; immunosuppressive; graft versus host disease; | |
| XX | transplant rejection; therapy; signal transduction. | |
| OS | Homo sapiens. | |
| XX | WO9839361-A1. | |
| PN | 11-SEP-1998. | |
| XX | PD | |
| XX | 03-MAR-1998; | 98WO-US04270. |
| PF | 03-MAR-1997; | 97US-0810572. |
| XX | (STUD-) ST JUDE CHILDREN'S RES HOSPITAL. | |
| PA | Bram RJ, Von Bulow G; | |
| XX | WPI; 1998-506346/43. | |
| XX | N-PSDB; AAV57330. | |
| DR | | |

```

XX New isolated transmembrane activator protein - used to develop
PT products for treating e.g. infections, cancers, autoimmune and
PT inflammatory conditions, transplant rejection or graft-versus-host
PT disease
XX
XX Claim 8, page 73, 89pp, English.
XX
XX This is the amino acid sequence of the N-terminal, i.e. the
CC extracellular, domain of novel human transmembrane activator and
CC CAML-interactor (TACI) protein (see AA075783). TACI is a lymphocyte
CC receptor protein that is involved in the calcium activation pathway.
CC It is normally present in B-lymphocytes, and to a much lesser extent
CC in immature T-lymphocytes, and can therefore be targeted to
CC specifically regulate B cell responses without affecting T cell
CC activity. The extracellular domain of TACI functions as a binding
CC site for a ligand that stimulates the activation of the cell by
CC inducing the binding of the C-terminal portion (see AA075784) of
CC TACI to the N-terminal domain of CAML. A recombinant form of the
CC extracellular portion of TACI acts as a dominant-negative or
CC blocking agent and acts to suppress the immune system. It can be
CC used to treat or prevent autoimmune disease, graft rejection or
CC graft versus host disease. The extracellular region is also used
CC in a claimed method for identifying a ligand for TACI, in which
CC binding of a candidate molecule is determined by detecting cellular
CC activation of the AP-1, CAMP or NF-KB pathway, of NF-AT
CC transcription factor, or of NF-AT dependent transcription.
CC
XX Sequence 166 AA:
SQ
Query Match 100.0%; Score 909, DB 19, Length 166;
Best Local Similarity 100.0%; Pred. No. 2,8e-83;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSGLSRRGRGRSRVDOERFPQGLMTGVAMRSCEPEQYMDPLGTGCMCKTICNHQSQR 60
DB 1 MSGLSRRGRGRSRVDOERFPQGLMTGVAMRSCEPEQYMDPLGTGCMCKTICNHQSQR 60
QY 61 TCAACFRSLSCRKEQGFYDHLNRDLCISGQHPKQCAVFCENKLRSPVNLPEELRR 120
DB 61 TCAACFRSLSCRKEQGFYDHLNRDLCISGQHPKQCAVFCENKLRSPVNLPEELRR 120
QY 121 QRSGEVNNSDNSGRYQGLEHRSSEASPALPGIKLSADQVALVYST 166
DB 121 QRSGEVNNSDNSGRYQGLEHRSSEASPALPGIKLSADQVALVYST 166
DB 121 QRSGEVNNSDNSGRYQGLEHRSSEASPALPGIKLSADQVALVYST 166

RESULT 2
AAE15494
ID AAE15494 standard; Protein; 166 AA.
XX
XX AAE15494;
AC
XX
XX 12-MAR-2002 (first entry)
DT
XX
XX Human TACI extracellular domain.
DE
XX
XX Human; transmembrane activator and intracellular CAML interactor; TACI;
KW cytoactive; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW prostate; inflammatory; immune disorder; diarrhoea; psoriasis; colitis;
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis.
XX
XX Homo sapiens.
OS
XX
XX WO200187979-A2.
XX
XX 22-NOV-2001.
XX
XX 14-MAY-2001; 2001WO-US15567.
XX

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XX
XX 12-MAY-2000; 2000US-204039P.
PR
XX 27-JUN-2000; 2000US-214591P.
PR
XX 14-MAY-2001; 2001US-0214591.
XX
XX (AMGE-) AMGEN INC.
XX
XX The111 LE, Yu G;
XX
XX WPI, 2002-066686/09.
XX
XX Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumour necrosis factor
PT family ligand
XX
XX Claim 1, Fig 12A, 94pp, English.
PS
XX
XX The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering
CC a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
CC family ligand), having the consensus sequence, but not the extracellular
CC region of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
CC is human TACI protein extracellular domain.
XX
XX Sequence 166 AA:
SQ
Query Match 100.0%; Score 909, DB 23; Length 166;
Best Local Similarity 100.0%; Pred. No. 2,8e-83;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSGLSRRGRGRSRVDOERFPQGLMTGVAMRSCEPEQYMDPLGTGCMCKTICNHQSQR 60
DB 1 MSGLSRRGRGRSRVDOERFPQGLMTGVAMRSCEPEQYMDPLGTGCMCKTICNHQSQR 60
QY 61 TCAACFRSLSCRKEQGFYDHLNRDLCISGQHPKQCAVFCENKLRSPVNLPEELRR 120
DB 61 TCAACFRSLSCRKEQGFYDHLNRDLCISGQHPKQCAVFCENKLRSPVNLPEELRR 120
QY 121 QRSGEVNNSDNSGRYQGLEHRSSEASPALPGIKLSADQVALVYST 166
DB 121 QRSGEVNNSDNSGRYQGLEHRSSEASPALPGIKLSADQVALVYST 166

RESULT 3
AAE09244
ID AAE09244 standard; Protein; 265 AA.
XX
XX AAE09244;
AC
XX
XX 19-NOV-2001 (first entry)
DT
XX
XX Human TACI splice variant protein.
DE
XX
XX Human; TNF, tumour necrosis factor; TALL-1; APRIL; TNF receptor;
KW TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;
KW psoriasis.
XX
XX Homo sapiens.
OS
XX

```

XX WO200160397-A1.
 XX 23-AUG-2001.
 XX 26-NOV-2000; 2000WD-US32378.
 XX 16-FEB-2000; 2000UB-0182938.
 XX 22-AUG-2000; 2000UB-0226986.
 XX (GETH) GENENTECH INC.
 XX Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Maresters SA, Picetti RM,
 XX Yan M;
 XX WPI; 2001-541628/60.
 XX
 XX Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
 XX activity, for treating autoimmune disorders and cancer, comprises
 XX exposing the cells to TALL-1 or APRIL polypeptide agonists or
 XX antagonists -
 XX
 XX Example 1; Fig 6; 160pp; English.
 XX
 XX The invention relates to methods of using one or more agonists or
 XX antagonists to modulate the activity of the members of TNF (tumour
 XX necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR)
 XX e.g. TACI or BCMA. The method is useful for treating pathological
 XX conditions or diseases associated with increased TALL-1 and APRIL
 XX expression or activity. TALL-1 and APRIL antagonists are used to
 XX block the interaction between APRIL and TALL-1 with TACI or BCMA.
 XX They are useful for treating a mammal suffering from cancer such
 XX as leukaemia, lymphoma, myeloma, cancers of lung and colon and
 XX autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis,
 XX psoriasis and lupus erythematosus. The present sequence is human
 XX TACI splice variant protein.
 XX
 XX Sequence 265 AA;
 XX
 XX Query Match 100.0%; Score 909; DB 22; Length 265;
 XX Best Local Similarity 100.0%; Pred. No. 4,9e-83;
 XX Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1 MSGIGRSRRGRSRVDQERFPQGLMTGVAMRSCPEEYWDPLDGTGMSCKTICNHQSOR 60
 XX 1 MSGIGRSRRGRSRVDQERFPQGLMTGVAMRSCPEEYWDPLDGTGMSCKTICNHQSOR 60
 XX
 XX 61 TCAAFCRSLSCRKQKGYDHLRDICISCASTCGQHPKQCAVFCENKLRSPVNLPEELRR 120
 XX 61 TCAAFCRSLSCRKQKGYDHLRDICISCASTCGQHPKQCAVFCENKLRSPVNLPEELRR 120
 XX
 XX 121 QRSGEVENNSDNGRKYQGLEHGRSEASPALPELKLISADQVALVYST 166
 XX 121 QRSGEVENNSDNGRKYQGLEHGRSEASPALPELKLISADQVALVYST 166
 XX
 XX RESULT 4
 XX AAW75783
 XX ID AAW75783 standard; Protein; 293 AA.
 XX
 XX AAW75783;
 XX
 XX 18-JAN-1999 (first entry)
 XX
 XX Human lymphocyte surface receptor TACI.
 XX
 XX TACI; transmembrane activator and CAML-interactor;
 XX calcium signal-modulating cyclophilin ligand; human;
 XX lymphocyte surface receptor; human; B-cell; B lymphocyte;
 XX infection; cancer; rheumatoid arthritis; autoimmune disease;
 XX glomerulonephritis; immunosuppressive; graft versus host disease;
 XX transplant rejection; therapy.

OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX
 XX Domain 1..166
 XX /label= Extracellular_domain
 XX /note= "Claim 8"
 XX
 XX Domain 167..186
 XX /label= Transmembrane_domain
 XX /note= "Claim 6"
 XX
 XX Domain 187..294
 XX /label= Cytoplasmic_domain
 XX /note= "Claim 6"
 XX
 XX Peptide 34..71
 XX /note= "TNFR_NGFR motif"
 XX
 XX WO9839361-A1.
 XX
 XX 11-SEP-1998.
 XX
 XX 03-MAR-1998; 98WO-US04270.
 XX
 XX 03-MAR-1997; 97US-0810572.
 XX
 XX (STUD-) ST JUDE CHILDREN'S RES HOSPITAL.
 XX
 XX Bram RJ, Von Bulow G;
 XX
 XX WPI; 1998-506346/43.
 XX
 XX N-PSDB; AAV57328.
 XX
 XX New isolated transmembrane activator protein - used to develop
 XX products for treating e.g. infections, cancers, autoimmune and
 XX inflammatory conditions, transplant rejection or graft-versus-host
 XX disease
 XX
 XX Claim 20; Fig 2a; 89pp; English.
 XX
 XX This is the amino acid sequence of novel human transmembrane
 XX activator and CAML-interactor (TACI) protein, a lymphocyte receptor
 XX protein that is involved in the calcium activation pathway. TACI
 XX is normally present in B-lymphocytes, and to a much lesser extent
 XX in immature T-lymphocytes, and can therefore be targeted to
 XX specifically regulate B cell responses without affecting T cell
 XX activity. TACI cDNA (seeV57328) was isolated from a B-lymphocyte
 XX cDNA library using a yeast two-hybrid assay. Also claimed are
 XX the C-terminal (see AAW75784) and N-terminal (see AAW75785) fragments
 XX of TACI, recombinant DNA constructs, unicellular hosts, and
 XX antibodies to TACI protein. Methods are claimed for identifying a
 XX ligand for TACI and for identifying immunosuppressive drugs that
 XX selectively block the action of B lymphocytes without affecting
 XX mature T lymphocytes. TACI can be activated to increase immune
 XX system activity, e.g. for treating infections or cancers. It can
 XX be blocked to provide immunosuppression, e.g. for treating
 XX autoimmune and inflammatory conditions such as immune complex-
 XX induced vasculitis, glomerulonephritis, haemolytic anaemia,
 XX myasthenia gravis, type II collagen-induced arthritis, experimental
 XX allergic and hyperacute xenograft rejection, rheumatoid arthritis,
 XX systemic lupus erythematosus, transplant rejection, cancer or
 XX graft versus host disease.
 XX
 XX Sequence 293 AA;
 XX
 XX Query Match 100.0%; Score 909; DB 19; Length 293;
 XX Best Local Similarity 100.0%; Pred. No. 5,6e-83;
 XX Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1 MSGIGRSRRGRSRVDQERFPQGLMTGVAMRSCPEEYWDPLDGTGMSCKTICNHQSOR 60
 XX 1 MSGIGRSRRGRSRVDQERFPQGLMTGVAMRSCPEEYWDPLDGTGMSCKTICNHQSOR 60
 XX
 XX 61 TCAAFCRSLSCRKQKGYDHLRDICISCASTCGQHPKQCAVFCENKLRSPVNLPEELRR 120
 XX 61 TCAAFCRSLSCRKQKGYDHLRDICISCASTCGQHPKQCAVFCENKLRSPVNLPEELRR 120

Qy 121 ORSGEVENNSDNGRYQGLEHRSSEASPALPGIKLSADQVALVYST 166
Db 121 ORSGEVENNSDNGRYQGLEHRSSEASPALPGIKLSADQVALVYST 166

RESULT 5
ID AAB36312 standard; Protein; 293 AA.
XX AAB36312;
XX
XX
XX 26-FEB-2001 (first entry)
XX
XX
XX Human neutrokin-alpha binding protein TR17 SEQ ID NO:2.
XX
XX Human; neutrokin-alpha binding protein; NAR protein; TR17; cytostatic;
XX immunosuppressive; neutrotropic; neuroprotective; antiviral; antiallergic;
XX heparotrophic; antidiabetic; antiinflammatory; antitumor; cardiac;
XX ophthalmological; gene therapy; immunodeficiency disorder; diagnosis;
XX autoimmune disorder.
XX
XX Homo sapiens.
XX OS
XX WO200058362-A1.
XX
XX 05-OCT-2000.
XX
XX 24-MAR-2000; 2000WO-US07966.
XX
XX 26-MAR-1999; 99US-0126599.
XX 10-MAR-2000; 2000US-0188208.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Ullrich S, Baker K;
XX
XX WPI; 2000-602359/57.
XX N-PSDB; AAC64602.
XX
XX Nucleic acid encoding a neutrokin-alpha receptor (NAR) such as TR17,
XX useful for producing TR17 protein which is used in the treatment and
XX diagnosis of autoimmune and immunodeficiency disorders -
XX
XX Claim 1; Fig 1; 398pp; English.

The present sequence represents the human neutrokin-alpha binding (NAR)
protein designated TR17. TR17 has cytostatic, immunosuppressive,
neutrotropic, neuroprotective, antiviral, antiallergic, hepatotropic,
antidiabetic, antiinflammatory, antitumor, cardiac and ophthalmological
activities and can be used in gene therapy. The TR17 protein and
antibodies are useful for treating and diagnosing immunodeficiency
disorders and autoimmune disorders. The TR17 polypeptides,
polynucleotides, antibodies, agonists and/or antagonists are used for
treating various other diseases defined in the specification and as
research tools for studying the phenotypic effects that result from
inhibiting TR17/TR17 ligand interactions on various cell types.

Sequence 293 AA;
SQ

Query Match 100.0%; Score 909; DB 21; Length 293;
Best Local Similarity 100.0%; Pred. No. 5.6e-83;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSGLSRRRGGSRVQDERPQGLMTGVAMRSCPEBOYMDPLGTGCMCKITCNHQSQR 60
Db 1 MSGLSRRRGGSRVQDERPQGLMTGVAMRSCPEBOYMDPLGTGCMCKITCNHQSQR 60

Qy 61 TCNARCRSLSCRRKQGFYDHLRLDPCISGASICGHPKQCAVFCENKLRSPVNLPELRR 120
Db 61 TCNARCRSLSCRRKQGFYDHLRLDPCISGASICGHPKQCAVFCENKLRSPVNLPELRR 120

Qy 121 ORSGEVENNSDNGRYQGLEHRSSEASPALPGIKLSADQVALVYST 166
Db 121 ORSGEVENNSDNGRYQGLEHRSSEASPALPGIKLSADQVALVYST 166

Db 121 ORSGEVENNSDNGRYQGLEHRSSEASPALPGIKLSADQVALVYST 166
RESULT 6
ID AAY94000 standard; Protein; 293 AA.
XX AAY94000;
XX
XX
XX 20-OCT-2000 (first entry)
XX
XX
XX A transmembrane activator and CAML-interactor (TACI).
XX
XX
XX Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
XX transmembrane activator and CAML-interactor; tumor necrosis factor; TNF;
XX ztnf4 activity; antibody production; autoimmune disease; amyloidosis;
XX systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
XX rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
XX end stage renal failure; glomerulonephritis; vasculitis; nephritis;
XX renal neoplasia; multiple myeloma; lymphoma; light chain neuropathy;
XX immune response; immunosuppression; graft rejection; joint pain;
XX graft versus host disease; inflammation; swelling; anaemia; septic shock;
XX insulin dependent diabetes mellitus; Crohn's disease; hypertension;
XX renal artery stenosis; occlusion; cholesterol; renal emboli.

Homo sapiens.
OS
XX WO200040716-A2.
XX
XX 13-JUL-2000.
XX
XX 07-JAN-2000; 2000WO-US00396.
XX
XX 07-JAN-1999; 99US-0226533.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Gross JA, Xu W, Madden K, Yee DP;
XX
XX WPI; 2000-452538/39.
XX N-PSDB; AAA58558.
XX
XX Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,
XX renal disease, graft versus host disease, and inflammation, comprises
XX administering a BR43x2, TACI or BCMA extracellular domain polypeptide -
XX
XX Disclosure; Page 149-150; 175pp; English.

The present sequence represents a human transmembrane activator and
CAML-interactor (TACI) receptor. TACI is a tumour necrosis factor (TNF)
receptor. The extracellular domains of BR43x2 (an isoform of TACI), TACI
or BCMA (a related B cell protein) receptor contain a cysteine rich
domain, and are used for inhibiting ztnf4 activity. Ztnf4 is a TNF
ligand. They may also be used for inhibiting BR43x2, TACI or BCMA
receptor-ligand engagement associated with activated or resting B
lymphocytes, effector T-cells, or with antibody production. The
antibody production is associated with an autoimmune disease selected
from systemic lupus erythematosus, myasthenia gravis, multiple sclerosis
and rheumatoid arthritis. The ztnf4 activity and BR43x2, TACI or BCMA
receptor-ligand engagement is associated with asthma, bronchitis,
emphysema, end stage renal failure, glomerulonephritis, vasculitis,
nephritis, pyelonephritis, renal neoplasia, multiple myelomas, lymphomas,
light chain neuropathy, amyloidosis, moderating immune response,
immunosuppression, graft rejection, graft versus host disease,
inflammation, insulin dependent diabetes mellitus, Crohn's disease, joint
pain, swelling, anaemia, or septic shock. BR43x2, TACI, and BCMA
polypeptides, fusions, antibodies, agonists or antagonists can be used
to treat hypertension, renal artery stenosis, or occlusion, and
cholesterol or renal emboli.

Sequence 293 AA;
SQ

Query Match 100.0%; Score 909; DB 21; Length 293;

| Best Local Matches | Similarity | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
|--------------------|---|---------|--------------------|--------|------|
| QY | 1 MSGLRSRRGGSR | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| Db | 1 MSGLSRRSGGSR | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| QY | 61 TCAAFCRSLSCREKQKFPYDHLRLDPCISGASICGHPKQCAVFCENKLRSPVNLPEELRR | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| Db | 61 TCAAFCRSLSCREKQKFPYDHLRLDPCISGASICGHPKQCAVFCENKLRSPVNLPEELRR | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| QY | 121 QRSGEVNNSDNSERYQGLEHRSSESPALPGLKLSADQVALVYST | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| Db | 121 QRSGEVNNSDNSERYQGLEHRSSESPALPGLKLSADQVALVYST | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| RESULT 7 | AAE09240 | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| ID | AAE09240 | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| AC | AAE09240 | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| XX | AAE09240 | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| XX | AAE09240 | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| DT | 19-NOV-2001 (first entry) | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| XX | Human TACI protein. | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| DE | Human TACI protein. | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| XX | Human, TNF, tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR; TACI; BCMA; therapy; cancer; leukemia; myeloma; lymphoma; autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis. | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| XX | Homo sapiens. | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| OS | Homo sapiens. | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| XX | MO200160397-A1. | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| PN | MO200160397-A1. | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| XX | 23-AUG-2001. | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| PD | 23-AUG-2001. | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| XX | 28-NOV-2000; 2000MO-US32378. | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| PF | 28-NOV-2000; 2000MO-US32378. | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| XX | 16-FEB-2000; 2000US-0182938. | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| PR | 16-FEB-2000; 2000US-0182938. | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| XX | 22-AUG-2000; 2000US-0226986. | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| PR | 22-AUG-2000; 2000US-0226986. | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| XX | (GETH) GENENTECH INC. | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| PA | (GETH) GENENTECH INC. | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| XX | Ashekzenzi AJ, Dodge KH, Grewal I, Kim KU, Marsters SA, Pitri RM, Yan M; | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| PI | Ashekzenzi AJ, Dodge KH, Grewal I, Kim KU, Marsters SA, Pitri RM, Yan M; | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| XX | WPI, 2001-541628/60. | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| DR | WPI, 2001-541628/60. | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| XX | N-PSDB; AAD15901. | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| DR | N-PSDB; AAD15901. | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| XX | Example 1; Fig 1; 160pp; English. | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| PS | Example 1; Fig 1; 160pp; English. | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| XX | The invention relates to methods of using one or more agonists or antagonists to modulate the activity of the members of TNF (tumour necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g. TACI or BCMA. The method is useful for treating pathological conditions or diseases associated with increased TALL-1 and APRIL expression or activity. TALL-1 and APRIL antagonists are used to block the interaction between APRIL and TALL-1 with TACI or BCMA. They are useful for treating a mammal suffering from cancer such as leukaemia, lymphoma, myeloma, cancers of lung and colon and autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The present sequence is human TACI protein. | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| CC | TACI protein. | 100.0%; | Pred. No. 5.6e-83; | Indels | Gaps |
| XX | Sequence | 293 AA; | | | |
| XX | Sequence | 293 AA; | | | |

| | | | | | | | | |
|----------|---|--|--------------------|--------------|-----------------|---------------|-----------|------|
| Beat | Local Similarity | 100.0%; | Pred. No. 5.6e-83; | Matches 166; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps |
| Qy | 1 | MSGLSRRSGRGRSRVDREPERFPGGLMTGTVMRSCPEBQYMDPLGLTMSCKTICNHQSQR | 60 | | | | | |
| Db | 1 | MSGLSRRSGRGRSRVDREPERFPGGLMTGTVMRSCPEBQYMDPLGLTMSCKTICNHQSQR | 60 | | | | | |
| Qy | 61 | TCAAFCRSLSCRKEQKGYDHLRLDTCISASCISQGHKQCAVFCENKLRSPVNLPELRR | 120 | | | | | |
| Db | 61 | TCAAFCRSLSCRKEQKGYDHLRLDTCISASCISQGHKQCAVFCENKLRSPVNLPELRR | 120 | | | | | |
| Qy | 121 | QSSGEVENNSDNGRYQGLERHGSBAPALPGLKLSADQVALYST | 166 | | | | | |
| Db | 121 | QSSGEVENNSDNGRYQGLERHGSBAPALPGLKLSADQVALYST | 166 | | | | | |
| RESULT 8 | | | | | | | | |
| AAV71914 | | | | | | | | |
| ID | AAV71914 | standard; Protein; 293 AA. | | | | | | |
| XX | AAV71914; | | | | | | | |
| AC | | | | | | | | |
| XX | | | | | | | | |
| DT | 26-MAR-2001 | (first entry) | | | | | | |
| DE | Human tumour necrosis factor receptor (TACI) protein. | | | | | | | |
| XX | | | | | | | | |
| KW | Human; transmembrane activator and CAML interactor; TACI; | | | | | | | |
| KW | tumour necrosis factor receptor; TNF; autoimmune disease; diabetes; | | | | | | | |
| KW | calcium-signal modulating cyclophilin ligand; CAML; viral infection; | | | | | | | |
| KW | neurotrophin alpha polypeptide; TACI-Ligand; TACI-L; cytostatic therapy; | | | | | | | |
| KW | neuroprotective; antidiabetic; antiviral; antiinflammatory; tumour; | | | | | | | |
| KW | antiarthritic; antirheumatic; immunosuppressive; multiple sclerosis; | | | | | | | |
| KW | rheumatoid arthritis; graft rejection; inflammation; cell proliferation; | | | | | | | |
| KW | cell death; immunoglobulin E-mediated allergic reaction; IGE. | | | | | | | |
| OS | Homo sapiens. | | | | | | | |
| XX | | | | | | | | |
| Key | Location/Qualifiers | | | | | | | |
| FT | Domain | 2..166 | | | | | | |
| FT | /label= Extracellular domain | | | | | | | |
| FT | /note= "Binds with amino acids 123-285 of extracellular domain of TACI-L" | | | | | | | |
| XX | WO20067034-A1. | | | | | | | |
| PN | | | | | | | | |
| XX | | | | | | | | |
| PD | 09-NOV-2000. | | | | | | | |
| XX | | | | | | | | |
| PF | 14-APR-2000; 2000WO-US10282. | | | | | | | |
| XX | | | | | | | | |
| PR | 30-APR-1999; 99US-0302863. | | | | | | | |
| XX | | | | | | | | |
| PA | (IMMU) IMMUNEX CORP. | | | | | | | |
| XX | | | | | | | | |
| PI | Goodwin RG, Din WS; | | | | | | | |
| XX | | | | | | | | |
| DR | WPI: 2001-016005/02. | | | | | | | |
| XX | | | | | | | | |
| XX | N-PSDB; AAD02006. | | | | | | | |
| PT | Use of new interactions between tumour necrosis factor receptors (TACI) | | | | | | | |
| PT | and TACI ligands to screen candidate molecules for determining agonist | | | | | | | |
| PT | and antagonist interactions which are used for treating inflammation - | | | | | | | |
| PS | Claim 10; Fig 1b; 46pp; English. | | | | | | | |
| XX | | | | | | | | |
| CC | The present sequence is a human tumour necrosis factor receptor (TACI) | | | | | | | |
| CC | protein. TACI (transmembrane activator and calcium-signal modulating | | | | | | | |
| CC | cyclophilin ligand (CAML)-interactor) forms a complex with neurotrophin | | | | | | | |
| CC | alpha polypeptide (TACI-Ligand). The antagonist or agonist of | | | | | | | |
| CC | TACI/TACI-L complex is useful for modulating an intracellular signalling | | | | | | | |
| CC | cascade mediated by TACI/TACI-L complex. Antagonists of TACI/TACI-L | | | | | | | |
| CC | complex are used to inhibit the interaction between TACI and TACI-L for | | | | | | | |
| CC | therapeutic purposes to treat tumour and tumour metastasis and to combat | | | | | | | |
| CC | various autoimmune diseases e.g. multiple sclerosis and diabetes, as | | | | | | | |

CC well as other disorders, such as viral infection, rheumatoid arthritis,
 CC graft rejection, and immunoglobulin (Ig) E-mediated allergic reactions
 CC and inflammation. The interaction is used to study cellular processes
 CC associated with tumour necrosis factor (TNF)-receptors such as immune
 CC regulation, cell proliferation, cell death and inflammatory responses.
 CC The interaction between the extracellular region of TACI and TACI-L can
 CC be used to further develop understanding of which cell types TACI-L
 CC acts upon.

XX Sequence 293 AA;

Query Match 100.0%; Score 909; DB 22; Length 293;
 Best Local Similarity 100.0%; Pred. No. 5.6e-83;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGIGRRRRGRRVDOERPPQGLMTGVMRSCPEBOYWDPLGTGCMSCKTICNHOSR 60
 DB 1 MSGIGRRRRGRRVDOERPPQGLMTGVMRSCPEBOYWDPLGTGCMSCKTICNHOSR 60
 QY 61 TCAAFCRSLSCRKEQGFYDHLRLDCISCSASICGHPKQCAVFCENKLRSPVNLPEELRR 120
 DB 61 TCAAFCRSLSCRKEQGFYDHLRLDCISCSASICGHPKQCAVFCENKLRSPVNLPEELRR 120
 QY 121 QRSGEVENNSDNGRYQGLFHRGSEASPALPGLKLSADQVALVYST 166
 DB 121 QRSGEVENNSDNGRYQGLFHRGSEASPALPGLKLSADQVALVYST 166

RESULT 9

AAU99512
 ID AAU99512 standard; Protein, 293 AA.

XX AAU99512;

DT 07-OCT-2002 (first entry)

DE Human TACI-IgG Fc fusion protein.

KW Human; tumour necrosis factor; TNF delta; pulmonary system disorder;
 KW immunoglobulin production; B-cell proliferation; immune system disorder;
 KW autoimmune disease; cancer; lymphoproliferative disorder; pain;
 KW microbial infection; parasitic infection; bone disease; atherosclerosis;
 KW cardiovascular disorder; neurodegenerative disease; wound healing;
 KW graft versus host disease; haematopoietic cell disorder; nephritis;
 KW transmembrane activator and CAML-interactor; TACI; TNF epsilon; IgG;
 KW immunoglobulin G; Fc portion.

XX Homo sapiens.

PN US2002064829-A1.

PD 30-MAY-2002.

PE 14-JUN-2001; 2001US-0879919.

PR 14-MAR-1996; 96US-016812P.

PR 15-JUN-2000; 2000US-211537P.

PR 23-OCT-2000; 2000US-241952P.

PR 13-DEC-2000; 2000US-254875P.

PR 16-MAR-2001; 2001US-276248P.

PR 23-MAR-2001; 2001US-277978P.

PR 25-MAY-2001; 2001US-293499P.

PR 12-MAR-1997; 97US-0815783.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Yu G, Ni J, Gentz RL, Dillon PJ,

DR WPI, 2002-556722/59.

XX Novel human multimeric tumour necrosis factor delta or epsilon protein

PT useful for treating disease or disorder of immune system such as

PT autoimmune disease, immunodeficiency, or cancer of immune system -

XX Example 29; Page 125; 143pp; English.

PS The present invention relates to the isolation of human tumour necrosis
 XX factor (TNF) delta and TNF epsilon proteins, and the polynucleotide
 CC sequences encoding them. The proteins are useful for modulating
 CC immunoglobulin production or for modulating proliferation of B-cells.
 CC The sequences of the invention are useful for treating diseases or
 CC disorders of the immune system. Such disorders include autoimmune
 CC diseases (e.g. systemic lupus erythematosus (SLE), acquired
 CC immunodeficiency syndrome (AIDS)), cancers of the immune system
 CC (e.g. chronic lymphocytic leukaemia (CLL), multiple myeloma,
 CC non-Hodgkin's lymphoma or Hodgkin's disease), lymphoproliferative
 CC disorders, microbial infections (e.g. viral, bacterial), parasitic
 CC infections, nephritis, bone disease (e.g. osteoporosis), atherosclerosis,
 CC pain, cardiovascular disorders (e.g. myocardial infarction, stroke),
 CC neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's
 CC disease), graft versus host disease, wound healing, haematopoietic cell
 CC disorders (e.g. anaemia), inflammatory disorders (e.g. asthma),
 CC diseases or disorders associated with various mucous membranes of the
 CC body (e.g. mucositis), and disorders of the pulmonary system. The
 CC proteins are also useful as a vaccine adjuvant that enhances immune
 CC responsiveness to specific antigens. The present sequence for human
 CC transmembrane activator and CAML-interactor (TACI)-immunoglobulin G
 CC (IgG) Fc fusion protein is used in the examples of the present
 CC invention.

XX Sequence 293 AA;

Query Match 100.0%; Score 909; DB 23; Length 293;
 Best Local Similarity 100.0%; Pred. No. 5.6e-83;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGIGRRRRGRRVDOERPPQGLMTGVMRSCPEBOYWDPLGTGCMSCKTICNHOSR 60
 DB 1 MSGIGRRRRGRRVDOERPPQGLMTGVMRSCPEBOYWDPLGTGCMSCKTICNHOSR 60
 QY 61 TCAAFCRSLSCRKEQGFYDHLRLDCISCSASICGHPKQCAVFCENKLRSPVNLPEELRR 120
 DB 61 TCAAFCRSLSCRKEQGFYDHLRLDCISCSASICGHPKQCAVFCENKLRSPVNLPEELRR 120
 QY 121 QRSGEVENNSDNGRYQGLFHRGSEASPALPGLKLSADQVALVYST 166
 DB 121 QRSGEVENNSDNGRYQGLFHRGSEASPALPGLKLSADQVALVYST 166

RESULT 10

ABB81488
 ID ABB81488 standard; Protein, 293 AA.

AC ABB81488;

DT 02-SEP-2002 (first entry)

DE Human TACI receptor related protein SEQ ID NO:8.

KW Human; Znftr12; tumour necrosis factor receptor; cytosolic;
 KW immunosuppressive; dermatological; antiinflammatory; antidiabetic;
 KW neuroprotective; antirheumatic; antiarthritic; antiaesthetic;
 KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
 KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
 KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;
 KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
 KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
 KW pyelonephritis; renal neoplasia; multiple myeloma; amyloidosis;
 KW light chain neuropathy; hypertension; large vessel disease;
 KW graft-versus host disease; graft rejection; Crohn's disease.

XX Homo sapiens.

PN WO200238766-A2.

XX 16-MAY-2002.

XX PF 05-NOV-2001; 2001WD-US47018.
 XX 07-NOV-2000; 2000US-246449P.
 PR 20-DEC-2000; 2000US-257131P.
 PR 28-JUN-2001; 2001US-301715P.
 PR 29-AUG-2001; 2001US-315565P.
 XX (ZYMO) ZYMOGENETICS INC.
 PA Gross JA, Xu W, Henne RM, Grant FU;
 PI WPI; 2002-508212/54.
 DR Novel isolated human tumor necrosis factor receptor polypeptide, termed
 XX Zentrif 12, useful for treating autoimmune disorders, emphysema, end
 PT stage renal failure or renal disease and lymphoma
 XX Disclosure; Page 136-137; 154pp; English.
 PS The present invention describes a human tumour necrosis factor receptor
 CC designated Zentrif12 (I). (I) has cytostatic, immunosuppressive,
 CC dermatological, antiinflammatory, neuroprotective, antidiabetic,
 CC antineumatic, antirheumatic, antiaesthetic, nephrotropic and hypotensive
 CC activities, and can be used in gene therapy. (I) can be used for
 CC inhibiting, in a mammal, the activity of a ligand that binds Zentrif12
 CC (e.g. ZTNF4), for treating disorders and diseases associated with B
 CC lymphocytes, activated B lymphocytes or reacting B lymphocytes, and for
 CC inhibiting the proliferation of tumour cells. (I) is useful for treating
 CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
 CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
 CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
 CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
 CC leukaemia, nephritis, and pyelonephritis, and for treating renal
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
 CC amyloidosis, hyperkension, large vessel diseases, graft-versus host
 CC disease, graft rejection and Crohn's disease. (I) is useful for
 CC modulating the immune system, for regulating B cell responses and
 CC development, for modulating development of other cells, antibody
 CC production and cytokine production, and for modulating T and B cell
 CC communication. The present sequence represents a protein which is
 CC given in the exemplification of the present invention.
 XX SQ Sequence 293 AA;
 Query Match 100.0%; Score 909; DB 23; Length 293;
 Best Local Similarity 100.0%; Pred. No. 5.6e-83;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSGGSRSRGGRSVYDQERFPQGLMTGVAMRSCPEBOYMDPLGTGCMSCKTI CNHOSOR 60
 Db 1 MSGGSRSRGGRSVYDQERFPQGLMTGVAMRSCPEBOYMDPLGTGCMSCKTI CNHOSOR 60
 QY 61 TCAAFCRSLSCRKQKGRKYDHLRDCISCASICGQHPKQCAVFCENKLRSPVNPPELRR 120
 Db 61 TCAAFCRSLSCRKQKGRKYDHLRDCISCASICGQHPKQCAVFCENKLRSPVNPPELRR 120
 QY 121 QRSGEVENNSDNGRYOGL EHRGSEASPALPGKLSDQVALVYST 166
 Db 121 QRSGEVENNSDNGRYOGL EHRGSEASPALPGKLSDQVALVYST 166
 RESULT 11
 AA014130
 ID AA014130 standard; Protein: 293 AA.
 XX AA014130;
 AC
 XX 02-MAY-2002 (first entry)
 DT
 XX Human transmembrane activator CAML interactor protein (TACI).
 DE Human transmembrane activator CAML interactor protein; TACI; cytostatic;
 KW Human transmembrane activator CAML interactor protein; TACI; cytostatic;

KW cell proliferation; tumour; vulnery; renal cell cancer; mastocytoma;
 KW Kaposi's sarcoma; breast; ovarian carcinoma; rectal; throat; melanoma;
 KW colon; bladder; mammary adenocarcinoma; gastrointestinal; hyperplasia;
 KW pharyngeal squamous cell; stomach; cellular hyperproliferation; pannus;
 KW scleroderma; rheumatoid arthritis; scarring; liver; lung fibrosis;
 KW uterine.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Domain 1..114
 FT label= Extracellular_domain
 XX
 XX W0200181417-A2.
 XX
 XX 01-NOV-2001.
 PD
 XX 27-APR-2001; 2001WO-US40626.
 PF
 XX 27-APR-2000; 2000US-199946P.
 PR
 XX (BIOJ) BIOGEN INC.
 PA (APOT-) APOTEC R & D SA.
 XX Ambrose C, Thompson J, Schneider P, Rennett P;
 PI WPI; 2002-062027/08.
 DR N-PSDB; AAK98726.
 DR
 XX Treating mammal for condition associated with undesired cell
 PT proliferation e.g., solid tumour or reducing solid tumour size located in
 PT mammal comprises administering transmembrane activator CAML interactor
 PT protein reagent -
 XX
 PS Claim 8; Fig 1; 42pp; English.
 XX
 CC This sequence represents the human transmembrane activator CAML
 CC interactor protein (TACI). The invention relates to treating a mammal for
 CC a condition associated with undesired cell proliferation (e.g. a solid
 CC tumour, or reducing the size of a solid tumour located on or in a mammal)
 CC comprising administering a transmembrane activator CAML interactor
 CC protein (TACI) reagent. The TACI reagent has cytostatic and vulnery
 CC activity. Treating a mammal (e.g. human, cow, horse, dog, mouse, rat or
 CC cat) for a condition associated with undesired cell proliferation (e.g.
 CC sarcoma, ovarian carcinoma, rectal cancer, throat cancer, melanoma, colon
 CC cancer, bladder cancer, mastocytoma, lung cancer, mammary adenocarcinoma,
 CC pharyngeal squamous cell carcinoma, gastrointestinal cancer or stomach
 CC cancer). The method is also useful for treating cellular
 CC hyperproliferation (hyperplasia) such as scleroderma, pannus formation in
 CC rheumatoid arthritis, post-surgical scarring and lung, liver and uterine
 CC fibrosis. The TACI reagent of the invention can extend mean survival time
 CC of a mammal by 25% as compared to the mean survival time of a mammal in
 CC the absence of administering the TACI reagent. The TACI reagent also
 CC reduces the size of the tumour by 25% or more.
 XX SQ Sequence 293 AA;
 Query Match 100.0%; Score 909; DB 23; Length 293;
 Best Local Similarity 100.0%; Pred. No. 5.6e-83;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSGGSRSRGGRSVYDQERFPQGLMTGVAMRSCPEBOYMDPLGTGCMSCKTI CNHOSOR 60
 Db 1 MSGGSRSRGGRSVYDQERFPQGLMTGVAMRSCPEBOYMDPLGTGCMSCKTI CNHOSOR 60
 QY 61 TCAAFCRSLSCRKQKGRKYDHLRDCISCASICGQHPKQCAVFCENKLRSPVNPPELRR 120
 Db 61 TCAAFCRSLSCRKQKGRKYDHLRDCISCASICGQHPKQCAVFCENKLRSPVNPPELRR 120
 QY 121 QRSGEVENNSDNGRYOGL EHRGSEASPALPGKLSDQVALVYST 166
 Db 121 QRSGEVENNSDNGRYOGL EHRGSEASPALPGKLSDQVALVYST 166

RESULT 12
AAU75408
ID AAU75408 standard; Protein; 293 AA.
XX
AC AAU75408;
XX
DT 09-APR-2002 (first entry)
XX
DE Tumour necrosis factor (TNF) receptor TACI-Fc fusion.
XX
KM Tumour necrosis factor; TNF; cytostatic; arteriosclerosis;
KM analgesic; cerebroprotective; neurotrophic; hepatotropic;
KM immunoglobulin production; B cell proliferation; immunosuppressive;
KM HIV; human immunodeficiency virus; autoimmune disease; immunodeficiency;
KM Sjogren's syndrome; systemic lupus erythematosus; Hodgkin's disease;
KM common variable immunodeficiency; CVID; non-Hodgkin's lymphoma; AIDS;
KM acquired immunodeficiency virus; cancer; multiple myeloma; CLL;
KM chronic lymphocytic leukaemia; lymphoproliferative disorder;
KM bacterial infection; viral infection; osteoporosis; atherosclerosis;
KM pain; cardiovascular disorder; stroke; allergy; Alzheimer's disease;
KM neurodegenerative disease; inflammation; liver disease; cirrhosis;
KM cardiomyopathy; diabetes; asthma; psoriasis; glomerulonephritis;
KM ulcerative colitis; angiogenesis; septic shock; wound healing;
KM tumour necrosis factor receptor; TACI; immunoglobulin; IgG.
XX
OS Homo sapiens.
XX Synthetic.
XX WO200196528-A2.
XX
XX 20-DEC-2001.
XX
XX 14-JUN-2001; 2001WO-US19026.
XX
XX 15-JUN-2000; 2000US-211537P.
XX 23-OCT-2000; 2000US-241952P.
XX 13-DEC-2000; 2000US-254875P.
XX 16-MAR-2001; 2001US-276248P.
XX 23-MAR-2001; 2001US-277978P.
XX 25-MAY-2001; 2001US-293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Yu G, Ni J, Gentz RL, Dillon PJ, Hilbert D;
XX WPI, 2002-130727/17.
XX N-PSDB; ABK13415.
XX
XX Novel multimeric human tumour necrosis factor delta or epsilon protein
XX useful for treating cancer, immune system disorder, infection,
XX cardiovascular disorders, liver disease, cardiomyopathy, diabetes and
XX psoriasis -
XX
XX Example 29; Page 341-342; 344pp; English.
XX
XX The invention describes a multimeric human tumour necrosis factor (TNF)
XX delta or epsilon protein (I). (I) or a composition containing them (II)
XX are useful for modulating immunoglobulin production or proliferation of B
XX cells. (I) or (II) is useful for treating a disease or disorder of the
XX immune system, preferably an autoimmune disease (e.g. Sjogren's syndrome,
XX systemic lupus erythematosus or common variable immunodeficiency (CVID));
XX an immunodeficiency e.g. acquired immunodeficiency syndrome (AIDS);
XX cancer of the immune system (e.g. Hodgkin's disease, non-Hodgkin's
XX lymphoma, multiple myeloma and chronic lymphocytic leukaemia (CLL)); in
XX the diagnosis and treatment or prevention of cancer, lymphoproliferative
XX disorder, bacterial and viral infections, osteoporosis, atherosclerosis,
XX pain, cardiovascular disorders (e.g. stroke), allergy, inflammation,
XX neurodegenerative disease (e.g. Alzheimer's disease), liver disease (e.g.
XX cirrhosis), cardiomyopathy, diabetes, asthma, psoriasis, septic shock,
XX glomerulonephritis, ulcerative colitis, arteriosclerosis, for promoting
XX angiogenesis and wound healing; as a diagnostic research reagent; as an

CC agent to target and kill cells expressing a TNFdelta and/or TNFepsilon
CC receptor; in apoptosis of transformed cell lines; mediation of cell
CC activation and proliferation; and as an immunogen to produce (ii). (ii)
CC is useful to purify, detect and target (I), for measuring levels of (I)
CC in biological samples, for immunophenotyping samples, and to treat,
CC inhibit or prevent diseases and disorders associated with aberrant
CC expression and/or activity of (I). This is the amino acid sequence of a
CC fusion protein of tumour necrosis factor receptor TACI and immunoglobulin
CC G (IgG) crystallisation fragment, described in the method of the
CC invention.
XX
SQ Sequence 293 AA;
XX
Query Match 100.0%; Score 909; DB 23; Length 293;
Best Local Similarity 100.0%; Pred. No. 5,6e-83;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSGGLRSRRGSRSDQERPPQGLMTGVNARSCEBEQYMPDLGTCMSCKTICNHQSOR 60
DB 1 MSGGLRSRRGSRSDQERPPQGLMTGVNARSCEBEQYMPDLGTCMSCKTICNHQSOR 60
QY 61 TCAAFCRSLSCRKEQKRYDHLRDCISCAISCGQHPKQCAVFCENKLRSPVNLPPELRR 120
DB 61 TCAAFCRSLSCRKEQKRYDHLRDCISCAISCGQHPKQCAVFCENKLRSPVNLPPELRR 120
QY 121 QRSGEVENNSDNGRYQGLIHRGSEASPALPQLKLSADQVALVYST 166
DB 121 QRSGEVENNSDNGRYQGLIHRGSEASPALPQLKLSADQVALVYST 166
XX
RESULT 13
AAE15493
ID AAE15493 standard; Protein; 293 AA.
XX
XX AAE15493;
XX
XX 12-MAR-2002 (first entry)
XX
XX Human transmembrane activator and intracellular CAML interactor protein.
XX
XX Human; transmembrane activator and intracellular CAML interactor; TACI;
XX cytoskeletal; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
XX lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
XX prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
XX drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
XX Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
XX human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
XX rheumatoid arthritis; atherosclerosis.
XX
XX Homo sapiens.
XX
XX Key location/Qualifiers
XX Region 34..66 /note= "Cysteine-rich consensus region"
XX Region 71..104 /note= "Cysteine-rich consensus region"
XX Domain 167..186 /label= Transmembrane_domain
XX
XX WO200187979-A2.
XX
XX 22-NOV-2001.
XX
XX 14-MAY-2001; 2001WO-US15567.
XX
XX 12-MAY-2000; 2000US-204039P.
XX 27-JUN-2000; 2000US-214591P.
XX 14-MAY-2001; 2001US-0214591.
XX
XX (AMGE-) AMGEN INC.
XX
XX The11 LE, Yu G;
XX

DR WPI: 2002-066686/09.
 XX Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor
 PT family ligand -
 XX
 XX Disclosure; Fig 12A, 94pp; English.
 XX
 CC The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering
 CC a specific binding partner for APRIL (G70, a tumor necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC antitumoral, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human TACI protein.
 XX
 SQ Sequence 293 AA;
 Query Match 100.0%; Score 909; DB 23; Length 293;
 Best Local Similarity 100.0%; Pred. No. 5.6e-83;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSGGSRSGRSRYDOEREPQGLMTGVAMRSCPEBOYMDPLGTCSCKTICNHQSOR 60
 DB 1 MSGGSRSGRSRYDOEREPQGLMTGVAMRSCPEBOYMDPLGTCSCKTICNHQSOR 60
 QY 61 TCAAFCRSLSCRKQEGKYDHLNDICISCAICGHPKQCAVFCENKLRSPVNLPEELRR 120
 DB 61 TCAAFCRSLSCRKQEGKYDHLNDICISCAICGHPKQCAVFCENKLRSPVNLPEELRR 120
 QY 121 QRSGEVNNSDNSGRYQGLFHRGSEASPALPGLKLSADQVALVYST 166
 DB 121 QRSGEVNNSDNSGRYQGLFHRGSEASPALPGLKLSADQVALVYST 166
 RESULT 14
 ID AAV09900 standard; Protein; 293 AA.
 XX
 AC AAV09900;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human AGP-3 related protein receptor.
 XX
 KW Human; AGP-3; anti-inflammatory; antiarthritic; immunosuppressive;
 KW dermatological; neuroprotective; nootropic; immunomodulator; metabolic;
 KW antidiabetic; analgesic; nephrotropic; osteoplastic; cytotoxic; fever;
 KW antiparkinsonian; antipneumatic; vasotropic; antibacterial; asthma;
 KW AGP-3 receptor; tumor necrosis factor ligand family; AGP-3 receptor;
 KW meenteric lymph node; AGP-3R; inflammatory disease; immune disorder;
 KW rheumatoid arthritis; graft-versus-host disease; Crohn's disease;
 KW pancreatitis; amyotrophic lateral sclerosis; ALS; Alzheimer's disease;
 KW diabetes; glomerulonephritis; inflammatory bowel disease; ischemia;
 KW multiple sclerosis; Parkinson's disease; transgenic animal.
 XX
 OS Homo sapiens.
 XX
 XX WO200185782-A2.

PD 15-NOV-2001.
 XX
 XX 12-FEB-2001; 2001WO-US04568.
 XX
 PR 11-FEB-2000; 2000US-101800P.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Boyle WJ, Heu H;
 XX
 DR WPI: 2002-049441/06.
 DR N-PSDB; AAS18558.
 XX
 PT Composition, useful for identifying modulator of receptor for treating
 PT asthma and glomerulonephritis, comprises AGP-3 (tumor necrosis factor
 PT ligand family member) receptor and encoding nucleic acids -
 XX
 PS Disclosure; Page 117-119, 124pp; English.
 XX
 CC The invention relates to a composition (I) comprising AGP-3 receptor
 CC (tumor necrosis factor ligand family member) related protein (II)
 CC attached to a vehicle protein. (I) is useful for modulating AGP-3-related
 CC activity in mesenteric lymph nodes (MLN) of a mammal. (II) is useful in
 CC assays to identify cells and tissues that express AGP-3R or proteins
 CC related to AGP-3R-related protein and for identifying compounds
 CC (agonists or antagonists) that interact with AGP-3R proteins. (II) is
 CC also useful for identifying intracellular proteins that interact with
 CC the respective cytoplasmic domains by yeast two-hybrid screening
 CC process. (II) is involved in B cell growth, survival and activation
 CC particularly in lymph node, spleen, and Peyer's patches. AGP-3R
 CC agonists and antagonists identified using (II) are used for modulating
 CC B cell response and are used to treat diseases characterised by
 CC inflammatory processes or deregulated immune response such as
 CC rheumatoid arthritis, graft-versus-host disease, Crohn's disease,
 CC lupus, etc. (II) is also useful in the production of hybridoma cells
 CC which are derived from B cells, which involves treating the hybridoma
 CC cells with (II). (II) is useful in the treatment of inflammatory
 CC conditions of joints, e.g., rheumatoid arthritis, osteoarthritis, etc.
 CC (II), its agonists or antagonists are useful for treating acute
 CC pancreatitis, amyotrophic lateral sclerosis (ALS), Alzheimer's disease,
 CC asthma, atherosclerosis, cachexia/anorexia, diabetes, fever,
 CC glomerulonephritis, inflammatory bowel disease, ischemic injury
 CC including cerebral ischaemia, multiple myeloma, multiple sclerosis,
 CC osteoporosis, Parkinson's disease, pain, reperfusion injury, septic
 CC shock, etc. The nucleic acids are also useful for developing transgenic
 CC animals expressing (II), which are useful for producing the polypeptides
 CC and for the study of in vivo biological activity. The present sequence
 CC represents the amino acid sequence of human AGP-3 related protein
 CC receptor.
 XX
 SQ Sequence 293 AA;
 Query Match 100.0%; Score 909; DB 23; Length 293;
 Best Local Similarity 100.0%; Pred. No. 5.6e-83;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSGGSRSGRSRYDOEREPQGLMTGVAMRSCPEBOYMDPLGTCSCKTICNHQSOR 60
 DB 1 MSGGSRSGRSRYDOEREPQGLMTGVAMRSCPEBOYMDPLGTCSCKTICNHQSOR 60
 QY 61 TCAAFCRSLSCRKQEGKYDHLNDICISCAICGHPKQCAVFCENKLRSPVNLPEELRR 120
 DB 61 TCAAFCRSLSCRKQEGKYDHLNDICISCAICGHPKQCAVFCENKLRSPVNLPEELRR 120
 QY 121 QRSGEVNNSDNSGRYQGLFHRGSEASPALPGLKLSADQVALVYST 166
 DB 121 QRSGEVNNSDNSGRYQGLFHRGSEASPALPGLKLSADQVALVYST 166
 RESULT 15
 ID AAO14135 standard; Protein; 312 AA.
 XX

AA014135;
02-MAY-2002 (first entry)
Protein of N-terminus FLAG-tagged human full length TACI from pJ57552.
Human transmembrane activator CAML interactor protein; TACI; cytostatic; Kaposi's sarcoma; tumour; vulnereary; renal cell cancer; mastocytoma; colon; bladder; mammary adenocarcinoma; gasterointestinal; hyperplasia; pharyngeal squamous cell; stomach; cellular hyperproliferation; pannus; scleroderma; rheumatoid arthritis; scarring; mean survival time; liver; lung fibrosis; uterine; a proliferation inducing ligand; N-terminus; pJ57552; APRIL-R2.
Homo sapiens.
Synthetic.
Key Location/Qualifiers
Misc-difference 302
/label= Xaa
/note= "Xaa is encoded by TAA"
MO200181417-A2.
01-NOV-2001.
27-APR-2001; 2001WO-US40626.
27-APR-2000; 2000US-199946P.
(BIOJ) BIOGEN INC.
(APOT-) APOTEC R & D SA.
Ambrose C, Thompson J, Schneider P, Rennert P;
WPI: 2002-062027/08.
N-PSDB; AAK98731.
Treating mammal for condition associated with undesired cell proliferation e.g., solid tumour or reducing solid tumour size located in mammal comprises administering transmembrane activator CAML interactor protein reagent -
Example 1; Fig 2; 42pp; English.
This sequence represents the protein of an N-terminus FLAG-tagged human full length TACI from pJ57552 (FLAG-tagged human APRIL-R2 (a proliferation inducing ligand)). The invention relates to treating a mammal for a condition associated with undesired cell proliferation (e.g., a solid tumour, or reducing the size of a solid tumour located on or in a mammal) comprising administering a transmembrane activator CAML interactor protein (TACI) reagent. The TACI reagent has cytostatic and vulnereary activity. Treating a mammal (e.g., human, cow, horse, dog, mouse, rat or cat) for a condition associated with undesired cell proliferation (e.g., cancer such as renal cell cancer, Kaposi's sarcoma, breast cancer, sarcoma, ovarian carcinoma, rectal cancer, throat cancer, melanoma, colon cancer, bladder cancer, mastocytoma, lung cancer, mammary adenocarcinoma, pharyngeal squamous cell carcinoma, gasterointestinal cancer or stomach cancer). The method is also useful for treating cellular hyperproliferation (hyperplasia) such as scleroderma, pannus formation in rheumatoid arthritis, post-surgical scarring and lung, liver and uterine fibrosis. The TACI reagent of the invention can extend mean survival time of a mammal by 25% as compared to the mean survival time of a mammal in the absence of administering the TACI reagent. The TACI reagent also reduces the size of the tumour by 25% or more.

| | | | |
|----|-----|---|-----|
| Qy | 2 | SGGRSRRGSGSRVDOEERPFQGLMTGYAMSCEBEQWYPLDGTMSCKTINHO\$ORT | 61 |
| Db | 10 | SGLGSRRGSGSRVDOEERPFQGLMTGYAMSCEBEQWYPLDGTMSCKTINHO\$ORT | 69 |
| Qy | 62 | CAAFGRSLSCREKQGFVDHLIRDCISCA\$ICGHPQCAFCGNKLR\$PNTLPPELRQ | 122 |
| Db | 70 | CAAFGRSLSCREKQGFVDHLIRDCISCA\$ICGHPQCAFCGNKLR\$PNTLPPELRQ | 128 |
| Qy | 122 | RSGEVNN\$D\$NGRYOGL\$EHRG\$EASPAL\$PGLKLSADQVALVYST | 166 |
| Db | 130 | RSGEVNN\$D\$NGRYOGL\$EHRG\$EASPAL\$PGLKLSADQVALVYST | 174 |

Search completed: February 4, 2003, 12:57:46
Job time : 44.3401 secs

GenCore version 5.1.3
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OM protein - protein search, using SW model

Run on: February 4, 2003, 12:53:41 / Search time 35.6194 Seconds
(without alignments)
960.257 Million cell updates/sec

Title: US-09-854-864-15

Perfect score: 909
Sequence: 1 MSGIGRSRGRSGRVDQEE.....SPALPGKLSADQVALVYST 166

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_rhnc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_prodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-----------|--------------------|
| 1 | 140 | 15.4 | 156 | 6 Q9N146 | Q9N146 macaca mla |
| 2 | 93 | 10.2 | 840 | 4 Q96H26 | Q96H26 homo sapien |
| 3 | 93 | 10.2 | 1240 | 4 Q15030 | Q15030 homo sapien |
| 4 | 91 | 10.0 | 1704 | 5 Q94446 | Q94446 chironomus |
| 5 | 89 | 9.8 | 839 | 5 Q10652 | Q10652 caenorhabdi |
| 6 | 89 | 9.8 | 1878 | 4 Q9UIP9 | Q9UIP9 homo sapien |
| 7 | 88.5 | 9.7 | 665 | 5 Q9W241 | Q9W241 drosophila |
| 8 | 88.5 | 9.7 | 676 | 5 Q8SW8 | Q8SW8 drosophila |
| 9 | 87.5 | 9.6 | 415 | 4 Q8TCB8 | Q8TCB8 homo sapien |
| 10 | 87 | 9.6 | 272 | 4 Q9BXV4 | Q9BXV4 homo sapien |
| 11 | 86.5 | 9.5 | 292 | 4 Q96K87 | Q96K87 homo sapien |
| 12 | 86.5 | 9.5 | 310 | 10 Q03108 | Q03108 triticum ae |
| 13 | 86.5 | 9.5 | 353 | 10 Q03107 | Q03107 triticum ae |
| 14 | 86 | 9.5 | 1299 | 5 Q26489 | Q26489 spodoptera |
| 15 | 85 | 9.4 | 267 | 13 Q919M0 | Q919M0 neoceratodu |
| 16 | 85 | 9.4 | 1137 | 4 Q9H8C1 | Q9H8C1 homo sapien |

| | | | | | |
|----|------|-----|-------|-----------|---------------------|
| 17 | 85 | 9.4 | 1918 | 4 Q9BQW7 | Q9BQW7 homo sapien |
| 18 | 85 | 9.4 | 1925 | 4 Q9P2E3 | Q9P2E3 homo sapien |
| 19 | 84.5 | 9.3 | 355 | 16 Q8ZDV4 | Q8ZDV4 yersinia pe |
| 20 | 84.5 | 9.3 | 598 | 11 Q8R151 | Q8R151 mus musculu |
| 21 | 84.5 | 9.3 | 702 | 5 Q9VH96 | Q9VH96 drosophila |
| 22 | 83 | 9.1 | 820 | 10 Q9FFK8 | Q9FFK8 arabidopsis |
| 23 | 83 | 9.1 | 13288 | 6 Q18758 | Q18758 sus scrofa |
| 24 | 82.5 | 9.1 | 913 | 4 Q96BP4 | Q96BP4 homo sapien |
| 25 | 82.5 | 9.1 | 1362 | 13 Q9PVZ4 | Q9PVZ4 xenopus lae |
| 26 | 82 | 9.0 | 239 | 13 Q90ZL0 | Q90ZL0 fuqu rubrip |
| 27 | 82 | 9.0 | 868 | 5 Q9Y1V3 | Q9Y1V3 polyandroca |
| 28 | 82 | 9.0 | 932 | 11 Q6Z030 | Q6Z030 mus musculu |
| 29 | 82 | 9.0 | 1650 | 11 Q9QVT6 | Q9QVT6 ratcus sp. |
| 30 | 81.5 | 9.0 | 316 | 11 Q9Z2H9 | Q9Z2H9 mus musculu |
| 31 | 81 | 8.9 | 567 | 4 Q8WU13 | Q8WU13 homo sapien |
| 32 | 81 | 8.9 | 704 | 3 Q74567 | Q74567 trichoderma |
| 33 | 81 | 8.9 | 1140 | 4 Q96K87 | Q96K87 homo sapien |
| 34 | 80 | 8.8 | 108 | 16 Q07571 | Q07571 bacillus su |
| 35 | 80 | 8.8 | 330 | 5 Q18118 | Q18118 caenorhabdi |
| 36 | 80 | 8.8 | 996 | 11 Q924X6 | Q924X6 mus musculu |
| 37 | 80 | 8.8 | 1664 | 5 Q9TVQ2 | Q9TVQ2 caenorhabdi |
| 38 | 80 | 8.8 | 1792 | 13 Q57484 | Q57484 gallus gall |
| 39 | 79.5 | 8.7 | 98 | 5 Q16939 | Q16939 arcylostroma |
| 40 | 79.5 | 8.7 | 593 | 10 Q9SEW4 | Q9SEW4 juglans reg |
| 41 | 79.5 | 8.7 | 1963 | 5 Q9VY56 | Q9VY56 drosophila |
| 42 | 79.5 | 8.7 | 2189 | 5 Q9BI05 | Q9BI05 elimeria ten |
| 43 | 79 | 8.7 | 217 | 11 Q9CSB2 | Q9CSB2 mus musculu |
| 44 | 79 | 8.7 | 269 | 17 Q29751 | Q29751 archaeoglob |
| 45 | 79 | 8.7 | 317 | 11 Q70524 | Q70524 cricetus |

ALIGNMENTS

| | | | | | |
|--|---------|----------------------------|------------------|--------|---------|
| RESULT 1 | | | | | |
| Q9N146 | | PREDIMINARY; | | PRT; | 156 AA. |
| ID Q9N146; | | | | | |
| AC Q9N146; | | | | | |
| DT 01-OCT-2000 (TREMBLrel. 15, Created) | | | | | |
| DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update) | | | | | |
| DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update) | | | | | |
| DE Transmembrane activator (Fragment). | | | | | |
| GN NF-AT. | | | | | |
| OS Macaca mulatta (Rhesus macaque). | | | | | |
| OC Eukaryota; Metazoa; Chordata; Vertebrata; Buteleostomi; | | | | | |
| OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae; | | | | | |
| OC Cercopitheidae; Macaca. | | | | | |
| OX NCBI_TaxID=9544; | | | | | |
| ON [1] | | | | | |
| RP SEQUENCE FROM N.A. | | | | | |
| RA Arredondo J; | | | | | |
| RT "Cytokine Signal Transduction Genes from Rhesus Macaque." | | | | | |
| RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases. | | | | | |
| DR EMBL; AF227558; AAF73400.1; -. | | | | | |
| FT NON TER | | | | | |
| FT SEQUENCE | 156 AA; | 16170 MW; | 8AD74E4D17D511D0 | CRC64; | |
| QY | 138 | GLEHRSRSPALPGKLSADQVALVYST | 166 | | |
| DB | 1 | GLEHRSRSPALPGKLSADQVALVYST | 29 | | |
| RESULT 2 | | | | | |
| Q96H26 | | PREDIMINARY; | | PRT; | 840 AA. |
| ID Q96H26; | | | | | |
| AC Q96H26; | | | | | |
| DT 01-DEC-2001 (TREMBLrel. 19, Created) | | | | | |
| DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update) | | | | | |
| DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update) | | | | | |

DE Similar to bromodomain adjacent to zinc finger domain, 2A
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPH;
RA Strausberg R;
RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC008965; AA008965.1; -.
DR InterPro; IPR001637; AT_hook.
DR InterPro; IPR001487; Bromodomain.
DR InterPro; IPR001965; ZnF_PHD.
DR Pfam; PF02178; AT_hook; 2.
DR Pfam; PF00439; bromodomain; 1.
DR Pfam; PF00628; PHD; 1.
DR PROSITE; PS50014; BROMODOMAIN_2; 1.
SQ
FT NON_TER 1
SQ SEQUENCE 840 AA; 94884 MW; 3f8147d9b7034b45 CRC64;

| | | | | |
|-----------------------|--------|------------------|-------|----------------------------------|
| Query Match | 10.2%; | Score 93; | DB 4; | Length 840; |
| Best Local Similarity | 25.8%; | Pred. No. 0.086; | | |
| Matches | 40; | Conservative | 17; | Mismatches 68; Indels 30; Gaps 7 |

[illegible]

RESULT 3
015030
ID 015030 PRELIMINARY; PRT; 1240 AA

DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE KIA00314 protein (Fragment).
GN KIA00314.
OS Homo sapiens (Human).
OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
OC Mammalia, Eutheria, Primates, Catarrhini, Homiidae, Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=97349984; PubMed=9205841;
RA Nagase T., Ishikawa K., Nakajima D., Ohira M., Seki N., Miyajima N.,
RA Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. VII.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.";
RL DNA Res. 4:141-150(1997).
DR EMBL: AB002312; BAA20773.1; -.
DR HSSP: Q92831; 1891.
DR InterPro: IPR000637, AT_hock.
DR InterPro: IPR001487, Bromodomain.
DR InterPro: IPR004022, DDT_dom.
DR InterPro: IPR001965, ZnF_PHD.
DR Pfam: PF02178; AT_hock; 3.
DR Pfam: PF00439; bromodomain; 1.
DR Pfam: PF02791; DDT; 1.
DR Pfam: PF00628; PHD; 1.
DR PRINTS: PR00929, ATHOOK.

DR PRINTS; PRO0503; BROMODOMAIN.
DR SMART; SMO0384; AT hook; 3.
DR SMART; SMO0297; BROMO; 1.
DR SMART; SMO0289; PHD; 1.
DR PROSITE; PS50014; BROMODOMAIN_2; 1.
FT NON_TER 1 1
FT SEQUENCE 1240 AA; 140417 MW; 20BBDF1AA6BC5A1 CRC64;

Query Match 10.2%; Score 93; DB 4; Length 1240;
 Best Local Similarity 25.8%; Pred. No. 0.13;
 Matches 40; Conservative 17; Mismatches 68; Indels 30; Gaps 7;

QY 22 PGLMTGVAARSCPBEQYNDPLLGTMCKTI--CNHSGQRCA-----AFCSLSLR 72
Db 961 PEGTTTETSYETTPRIWRWQTLERCSRSAQVCLIGLEERSIAEKSVNKVTCT-LVCR 1018
QY 73 KEQGRFDHLHRCICASCIG---QHPRQCA-----YFC-----ENKLRVSNLEP 116
Db 1019 KGDN---DEFLLLDCGDRGCHYICHRPMEAVPEGDWECTVCLAQVEGEPTQKPGPK 1075
QY 117 ELRRQRSGVEYNNSDNSGRVQGLGHEHSGSASALP 151
Db 1076 RGQRKRKGSYLNFSBGGRRRRRLTLNGRSSPAAG 1110

RESULT 4
Q94446
ID Q94446 PRELIMINARY; PRT; 1704 AA

| | |
|----|--|
| DT | 01-FEB-1997 (TrEMBLrel. 02, Created) |
| DT | 01-FEB-1997 (TrEMBLrel. 02, Last sequence update) |
| DT | 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) |
| DE | 220 kDa silk protein. |
| GN | sp220. |
| OS | Chironomus thummi (midge). |
| OC | Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; |
| OC | Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; |
| OC | Chironomidae; Chironomidae; Chironominae; Chironomus. |
| CX | NCBI_TaxID=7154; |
| RN | [1] |
| RP | SEQUENCE FROM N.A. |
| RA | TISSUE=Salivary gland; |
| RC | Case S.T., Cox C., Bell W.C., Hoffman R.T., Martin J., Hamilton R.; |
| RT | "extraordinary conservation of cysteines among homologous Chironomus |
| RT | silk proteins gp185 and gp220." |
| RL | Submitted (Apr-1996) to the EMBL/GenBank/DBJ databases. |
| DR | EMBL; U54641; AAA9804.1; - |
| DR | InterPro; IPR004153; CXCXC repeat. |
| DR | InterPro; IPR000561; EGF-like. |
| DR | InterPro; IPR000583; Melittin_nemat. |
| DR | Pfam; PF03128; CXCXC; 69. |
| DR | PRINTS; PR00876; MTNEMAR05F. |
| DR | PROSITE; PS00022; EGF_1; UNKNOWN 2. |
| DR | PROSITE; PS01186; EGF_2; UNKNOWN 1. |
| QO | SEQUENCE 1704 AA; 185746 MW; 3A3F02A47C8F1E28 CRC64; |

| | | | | |
|-----------------------|--------|-----------------|-------|----------------|
| Query Match | 10.0%; | Score 91; | DB 5; | Length 1704; |
| Best Local Similarity | 21.4%; | Pred. No. 0.32; | | |
| Matches | 31; | Conservative | 22; | Mismatches 44; |
| | | | | Indels 48; |
| | | | | Gaps 7; |

QY 32 RSCPEEBYWD-----PLLTGC-----MSKTIQNNH-----SQPTCAFC 66
 Db 1357 QTCEAGSWSMSQTCCSCATATKCTGAQFWCAKCKCVCVQVENCKSPKVDQTSQCQC 1416
 QY 67 -RLSLCKBE--GKEYDH-----LRLDCTSCASISGQHPKQC---AYF 103
 Db 1417 PKMNPPEKGECTAGRTWTDATCTEKCATVVPNCSEPMVFDQATCGCKGKCNKPKLPADKVM 1476
 QY 104 CENKLSPPVLLPELARQSRSEVEN 128
 Db 1477 CDKKCAVCSLPEPTQTCPYSGGQTVN 1501

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RESULT 5
Q10652 PRELIMINARY; PRT; 839 AA.
AC Q10652;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Zinc finger protein CEZF.
GN CEZF.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=96003854; PubMed=7568208;
RA Saha V., Chaplin T., Gregorini A., Ayton P., Young B.D.;
RT "The leukemia-associated-protein (LAP) domain, a cysteine-rich motif,
RT is present in a wide range of proteins, including MLT, APL10, and MLT6
RT proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 92:9737-9741(1995).
CC -1- SIMILARITY: CONTAINS A CYS-RICH (PHD-FINGER) DOMAIN SIMILAR TO
CC THOSE FROM HAT1.1, MAIZE HOX1A AND PARSLER PR1.
DR EMBL; U20555; AAC46918.1; -.
DR InterPro; IPR001965; Znf_PHD.
DR Pfam; PF00628; PHD; 1.
DR SMART; SM00249; PHD; 2.
KW DNA-binding; zinc-finger; Metal-binding.
FT DOMAIN 8 54 CYS-RICH (PHD-FINGER) .
FT ZN FING 619 655 LEUCINE ZIPPER.
FT ZN FING 127 151 POTENTIAL.
SQ SEQUENCE 839 AA; 89439 MW; AFEFFB9D1D35B48 CRC64;

Query Match 9.8%; Score 89; DB 5; Length 839;
Best Local Similarity 32.5%; Pred. No. 0.24;
Matches 27; Conservative 8; Mismatches 28; Indels 20; Gaps 5;

QY 34 CPEQYMPDLGTGMSG-KTICNHSQRTCAFCRSLSCKRQKQKPYDHLRDCISCASI 92
Db 130 CNEEPNDKAKCA-CMSCKSTCKRSHYTCAG-RKGLC--EEGAL----- 172
QY 93 CGQHPKQCAVFCENKLRSPNLP 115
Db 173 -SRNVKCGY-CENHLKKAINDP 193

RESULT 6
Q9UIF9 PRELIMINARY; PRT; 1878 AA.
AC Q9UIF9;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Bromodomain adjacent to zinc finger domain 2A.
GN BAZ2A.
OS Homo sapiens (Human) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20130112; PubMed=10662543;
RA Jones M.H., Hamana N., Nezu J., Shimane M.;
RT "A novel family of bromodomain genes."
RL Genomics 63:40-45(2000).
DR EMBL; AB032254; BAA89211.1; -.
DR HSSB; Q92831; 1891.
DR InterPro; IPR000637; AT hook.
DR InterPro; IPR001487; Bromodomain.
DR InterPro; IPR004022; DDT_dom.
DR InterPro; IPR001739; Methy1-CpG_bind.
DR InterPro; IPR001965; Znf_PHD.

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DR Pfam; PF02178; AT_hook; 4.
DR Pfam; PF00439; bromodomain; 1.
DR Pfam; PF02791; DDT; 1.
DR Pfam; PF01429; MBP; 1.
DR Pfam; PF00628; PHD; 1.
DR PRINTS; PR00503; BROMODOMAIN.
DR SMART; SM00384; AT_hook; 3.
DR SMART; SM00297; BROMO; 1.
DR SMART; SM00391; MBP; 1.
DR SMART; SM00249; PHD; 1.
DR PROSITE; PS50014; BROMODOMAIN 2; 1.
SQ SEQUENCE 1878 AA; 208639 MW; 12683AFE63A93A6 CRC64;

Query Match 9.8%; Score 89; DB 4; Length 1878;
Best Local Similarity 23.3%; Pred. No. 0.61;
Matches 37; Conservative 18; Mismatches 66; Indels 38; Gaps 6;

QY 22 PQGLTGYANRSCPEQYWDPLGTGMSCKTIC-----NHQSRTCAFCRS 68
Db 1599 PEGTTEISYEITPRIRIWRQTLQRCSAAHVCLGHLERSIAMEKSVNRYTC----- 1652
QY 69 LSCRKQKQKPYDHLRDCISCASITCG--QHPKCA-----YFC-----ENKLRSPV 112
Db 1653 LVCRKGN---DEFLLCDCGDRGCHYCHRPKMEAVPEGWFTVCLAAQYVEGFQKP 1709
QY 113 NLPELPRQSRSGVENNSDNGRYQGLEHRSSEASPALP 151
Db 1710 GPPKRGQKRGKSGYSLNPFSEGGRRRRVLLKGRSEPAAGP 1748

RESULT 7
Q9W241 PRELIMINARY; PRT; 665 AA.
AC Q9W241;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-OCT-2001 (TREMblrel. 18, Last annotation update)
DE CG12489 protein.
GN CG12489.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Archopoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brocksen P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieres S., Fleischmann W.,
RA Foster C., Gabriellian A.B., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gottell J.H., Gu Z., Guan X., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hoeltin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalaali M., Kalush F., Karen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laake P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Metkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

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RC TISSUE=PLACENTA;
RA Strauberg R.;
RL Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF251057; AA34947.1; -
DR EMBL; BC022367; AA422367.1; -
DR InterPro; IPR002174; Furin-like.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF00090; tsp_1; 1.
DR SMART; SM00261; FU; 2.
DR PROSITE; PS00209; TSP1; 1.
DR PROSITE; PS50092; TSP1; 1.
SQ SEQUENCE 272 AA; 30928 MW; CACAECGB7E761189 CRC64;

Query Match
Best Local Similarity 24.6%; Score 87; DB 4; Length 272;
Matches 42; Conservative 18; Mismatches 59; Indels 52; Gaps 11;

Qy 28 GVAMRSCPEBOYD--PLIGTCMSCKTICNHOSORTCAAFCRSLSCREQGFYDHL--- 82
Db 74 GVCSSCPGSGYGYGFRYPDINKCTCKKADCD---TC--FNNKF-CTKCKSGFYHLGKC 125
Qy 83 LRDC-----ISCASI-----CGQHPQCAV--FCENKLRSPV----- 112
Db 126 LDCPBGLEANNHTECVSIHCEVSEWNPSPCTKKGKTCGFKGTETRVREITIQHPSA 185
Qy 113 --NLPELRORSSEVENNSDNGR--YQGLEHR-----GSEASPALPLK 154
Db 186 KGNLCPTNETRKTCTVQRKKCKGKGRKKRKRKKKPKNKESKRALPDSK 236

RESULT 11
Q096K87 PRELIMINARY; PRT; 292 AA.
AC O96K87;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE CDNA FLJ14440 f1s, clone HEMBL1000915, weakly similar to
DE subtilisin-like protease PACE4 precursor (EC 3.4.21.-).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN NCB1_TaxID=9606;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=EMBRIO;
RA Itegal T., Oca T., Hayashi K., Sugiyama T., Oeuchi T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;
RT "NDO human cDNA sequencing project.";
RL Submitted (MAY-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AK027346; BAB5051.1; -
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF00090; tsp_1; 1.
DR SMART; SM00181; EGF; 1.
DR PROSITE; PS50092; TSP1; 1.
SQ SEQUENCE 292 AA; 33243 MW; 01E2774AC3DA46F8 CRC64;

Query Match
Best Local Similarity 9.6%; Score 87; DB 4; Length 292;
Matches 42; Conservative 18; Mismatches 59; Indels 52; Gaps 11;

Qy 28 GVAMRSCPEBOYD--PLIGTCMSCKTICNHOSORTCAAFCRSLSCREQGFYDHL--- 82
Db 74 GVCSSCPGSGYGYGFRYPDINKCTCKKADCD---TC--FNNKF-CTKCKSGFYHLGKC 125
Qy 83 LRDC-----ISCASI-----CGQHPQCAV--FCENKLRSPV----- 112
Db 126 LDCPBGLEANNHTECVSIHCEVSEWNPSPCTKKGKTCGFKGTETRVREITIQHPSA 185

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Qy 113 --NLPELRORSSEVENNSDNGR--YQGLEHR-----GSEASPALPLK 154
Db 186 KGNLCPTNETRKTCTVQRKKCKGKGRKKRKRKKKPKNKESKRALPDSK 236

RESULT 12
Q003108 PRELIMINARY; PRT; 310 AA.
AC Q003108;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Cachepsin B (Fragment).
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticaceae; Triticum.
OX NCB1_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VAR. CHINESE SPRING;
RX MEDLINE=93258430; Pubmed=1302642;
RA Cejudo F.J., Murphy G., Chino C., Baulcombe D.C.;
RT "A gibberellin-regulated gene from wheat with sequence homology to
RT cachepsin B of mammalian cells.";
RL Plant J. 2:937-948(1992).
DR EMBL; X66014; CAA46812.1; -
DR HSSP; P07689; IODO.
DR MEROPS; C01.049; -.
DR InterPro; IPR000668; Peptidase_C1.
DR InterPro; IPR000169; Shprot_acsite.
DR Pfam; PF00112; Peptidase_C1; 1.
DR PRINTS; PR00705; PAPA1N.
DR Prodom; PD000158; Peptidase_C1; 1.
DR PROSITE; PS00138; THIOL_PROTEASE_CYS; 1.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
KW Hydrolyase; Thiol protease.
FT NON TER 310
SQ SEQUENCE 310 AA; 33811 MW; 2DE6F3264BB228C3 CRC64;

Query Match
Best Local Similarity 9.5%; Score 86.5; DB 10; Length 310;
Matches 36; Conservative 12; Mismatches 63; Indels 35; Gaps 5;

Qy 22 PGLMTGVAMRSCPE-----EQYWDPLIGTCMSCKTICNHOSORTCAAFCRSLSCR 72
Db 80 PGLIAGVPIKIHPEMDLPKFFDARTQNS-----SCSTIGNILDGHCACAFPAVE 132
Qy 73 KEQGFYDHL-----LRDSCASICGHPKQCAVFCENKLRSPVNLPELRORSGE 125
Db 133 ALQRFCHLMMSSVLSVNDLLAC-----CGFLCSGCGNGGYISAMRYFRRGV 182
Qy 126 VENNNSDNGRYQGLEHRGSEASPALP 151
Db 183 VTRECDPYFDQTCQHPGCE--PAYP 206

RESULT 13
Q003107 PRELIMINARY; PRT; 353 AA.
AC Q003107;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Cachepsin B (Fragment).
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticaceae; Triticum.
OX NCB1_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VAR. CHINESE SPRING;

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RX MEDLINE=93258430; PubMed=1302642;
 RA Cejudo F.J., Murphy G., Chinoy C.,
 RT "A glibeterralin-regulated gene from wheat with sequence homology to
 RL cathepsin B of mammalian cells";
 DR Plant J. 2:937-948 (1992).
 DR EMBL; X66013; CAA46811.1; -
 DR HSSP; F07688; I0D0.
 DR MEROPS; C01.049; -
 DR InterPro; IPR000668; Peptidase_C1.
 DR InterPro; IPR000169; SHprot acitc.
 DR Pfam; PF00112; Peptidase_C1.1.
 DR PRINTS; PR00705; PAPA1N_C1.1.
 DR Prodom; PD000158; Peptidase_C1.1.
 DR PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
 DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
 KM Hydroxylase; Thiol protease.
 FT NON TER
 SQ SEQUENCE 353 AA; 38355 MW; A10E7C84ED46E44 CRC64;

Query Match 9.5%; Score 86.5; DB 10; Length 353;
 Best Local Similarity 24.7%; Pred. No. 0.18;
 Matches 36; Conservative 12; Mismatches 63; Indels 35; Gaps 5;

QY 22 PGGLTWGVAMRSCPE-----EYWDPLGTCMSCKTICNHSQRTCAAFCSLSGR 72
 DB 80 PGGLTWGVAMRSCPE-----EYWDPLGTCMSCKTICNHSQRTCAAFCSLSGR 72
 QY 73 KGGKGFYDHL-----LRDCTSCASICGQHPKQCAFCENKLRSPVNLPELRGRSGE 125
 DB 133 ALQDRCTHLNMSVSLVNDLAC-----CGFLGSGGNGGYPISANRYFRSGV 182
 QY 126 VENNDSNGRYQGLEHRSSEASPALP 151
 DB 183 VTBECDPYFDQTCQHPGCE--PAYP 206

RESULT 14

ID Q26489 PRELIMINARY; PRT; 1299 AA.

AC Q26489;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Endoprotease furin.
 GN FURIN.
 OS Spodoptera frugiperda (Fall armyworm).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera.
 OX NCBI_TaxID=7108;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SF9;
 RA Cieplik M., Klenk H.;
 RT "Cloning and functional characterization of FURIN from Spodoptera
 RT frugiperda (Sf9) cells";
 RL Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.
 DR EMBL; Z68888; CAA93116.1; -
 DR HSSP; Q9405; IMP.
 DR InterPro; IPR002174; Furin-like.
 DR InterPro; IPR002079; Peptidase_S8.
 DR Pfam; PF01483; P.1.
 DR Pfam; PF00082; Peptidase_S8.1.
 DR PRINTS; PR00723; SUBTILISIN.
 DR Prodom; PD000177; P_domain.1.
 DR SMART; SM00261; FU; 10.
 DR PROSITE; PS00136; SUBTILASE_ASP; 1.
 DR PROSITE; PS00137; SUBTILASE_HIS; 1.
 DR PROSITE; PS00138; SUBTILASE_SER; 1.
 KW Protease.
 SQ SEQUENCE 1299 AA; 142020 MW; 4C3799C7B8C572AB CRC64;

Query Match 9.5%; Score 86; DB 5; Length 1299;
 Best Local Similarity 25.0%; Pred. No. 0.87;
 Matches 39; Conservative 16; Mismatches 51; Indels 50; Gaps 9;

QY 22 PGGLTWGVAMRSCPEQYWDPLGTCMSCKTICNHSQRTCAAFCSLSCKRECKF--- 78
 DB 1104 PRFMDGLCNECLSGSYDATTSGTGRSCDASC-----RTCSG-----PEQFECT 1148
 QY 79 -----YDHLRDCISASICG-----QHPKQCAFCENKLRSPVNLPELRGRSGEVE 127
 DB 1149 TCSRPLRLRIDRLNNOCPCCSESGVNSTPPTDCC-CH-----PE-----NGECI 1192
 QY 128 NNSDNGRYQGLEHRSSEASPALPGLKLSADQVALV 163
 DB 1193 NSS-VAGKRRIEMGALHTAPSAD-----AAPSVAIV 1223
 RESULT 15
 QY19M0
 ID Q919M0 PRELIMINARY; PRT; 267 AA.
 AC Q919M0;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Proenkephalin.
 OS Neoceratodus forsteri (Australian lungfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Dipnoi; Ceratodontiformes; Ceratodontidae; Neoceratodus.
 OX NCBI_TaxID=7892;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RA MEDLINE=20417836; PubMed=10960597;
 RA Sollars C., Danielson P., Jose J.M.P., Dore R.M.;
 RT "Deciphering the origin of Met-enkephalin and Leu-enkephalin in lobe-
 RT fanned fish: cloning of Australian lungfish proenkephalin";
 RL Brain Res. 874:131-136 (2000).
 DR EMBL; AF232671; AAF44658.1; -
 DR InterPro; IPR000094; Opioid neurop.
 DR Pfam; PF01160; Opioid neurop.
 DR PRINTS; PR01028; OPIOIDPRCSR
 DR PROSITE; PS01252; OPIOIDS_PRECURSOR; UNKNOWN.1.
 SQ SEQUENCE 267 AA; 30688 MW; 69C92C0F3378E0F0 CRC64;

Query Match 9.4%; Score 85; DB 13; Length 267;
 Best Local Similarity 29.4%; Pred. No. 0.19;
 Matches 30; Conservative 7; Mismatches 35; Indels 30; Gaps 5;

QY 62 CAAFRSLSCKREQGFYDHLRDCISASICGQH---PKQCAFCENKLRSPVNLPELRGRSGEVE 110
 DB 15 CA--CLILAVRAECSK-----DCAHCTYHILGHADINPLSTLECGKLPVSRWDMC 65
 QY 111 -----PVNLPELRGRSGEVENNSDN-----SGRYQLHR 142
 DB 66 KELLQVGKPEIMQEGETASVENDKENDORMFARKYGGFMER 107

Search completed: February 4, 2003, 12:59:11
 Job time : 38.6194 secs

GenCore version 5.1.3
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OM protein - protein search, using SW model

Run on: February 4, 2003, 12:53:16 ; Search time 11.4251 Seconds
(without alignments)
602.627 Million cell updates/sec

Title: US-09-854-864-15

Perfect score: 909
Sequence: 1 MSGIGRSRRGSRVDQER.....SPALPGKLSADQVALVYST 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-------------|---------------------|
| 1 | 909 | 100.0 | 293 | T13X_HUMAN | O14836 homo sapien |
| 2 | 419.5 | 46.1 | 249 | T13X_MOUSE | Q96t35 mus musculu |
| 3 | 97.5 | 10.7 | 1877 | PCK5_MOUSE | Q04592 mus musculu |
| 4 | 89 | 9.8 | 867 | YMA2_CAEEL | P34447 caenorhabdi |
| 5 | 86 | 9.5 | 297 | XEDA_HUMAN | O9hav5 homo sapien |
| 6 | 83 | 9.1 | 971 | RECK_MOUSE | O9z0j1 mus musculu |
| 7 | 83 | 9.1 | 1150 | APMU_PIG | P12021 sus scrofa |
| 8 | 82.5 | 9.1 | 913 | PCK5_HUMAN | Q92824 homo sapien |
| 9 | 82 | 9.0 | 4660 | LRP2_RAT | P98158 rattus norv |
| 10 | 81 | 8.9 | 971 | RECK_HUMAN | O95980 homo sapien |
| 11 | 81 | 8.9 | 1124 | TIER2_HUMAN | O02763 homo sapien |
| 12 | 80.5 | 8.9 | 937 | PAC4_RAT | O63415 rattus norv |
| 13 | 79.5 | 8.7 | 1172 | LMB3_HUMAN | Q14751 homo sapien |
| 14 | 79.5 | 8.7 | 1984 | YL_DROME | Q14258 drosophila |
| 15 | 78.5 | 8.6 | 630 | Y147_HUMAN | O14258 homo sapien |
| 16 | 77.5 | 8.5 | 2871 | PBN1_MOUSE | O61554 mus musculu |
| 17 | 76.5 | 8.4 | 1680 | PUR2_DROME | P30432 drosophila |
| 18 | 76 | 8.4 | 603 | CPAI_MOUSE | O61129 mus musculu |
| 19 | 76 | 8.4 | 1877 | PCK5_PAT | P4413 rattus norv |
| 20 | 75.5 | 8.3 | 427 | YK15_YEAST | Q07954 homo sapien |
| 21 | 75 | 8.3 | 400 | LMB_HIRME | Q25092 hirtudo medi |
| 22 | 75 | 8.3 | 446 | FAT_MOUSE | P70375 mus musculu |
| 23 | 75 | 8.3 | 448 | EDAR_HUMAN | O9une0 homo sapien |
| 24 | 75 | 8.3 | 969 | PAC4_HUMAN | P29122 homo sapien |
| 25 | 75 | 8.3 | 2871 | PBN1_HUMAN | P35555 homo sapien |
| 26 | 75 | 8.3 | 4544 | LRP1_HUMAN | Q07954 homo sapien |
| 27 | 74.5 | 8.2 | 501 | TRA2_MOUSE | P53712 mus musculu |
| 28 | 74.5 | 8.2 | 773 | ITB1_BOVIN | P53712 bos taurus |
| 29 | 74 | 8.1 | 1125 | TIER2_BOVIN | O06807 bos taurus |
| 30 | 74 | 8.1 | 1426 | EGFR_DROME | P04412 drosophila |
| 31 | 74 | 8.1 | 2569 | LMA3_MOUSE | O61789 mus musculu |
| 32 | 73.5 | 8.1 | 775 | PINC_MOUSE | P35831 mus musculu |
| 33 | 73.5 | 8.1 | 798 | ITB1_MOUSE | P09055 mus musculu |

| | | | | | | |
|----|------|-----|------|---|------------|--------------------|
| 34 | 73.5 | 8.1 | 1693 | 1 | RIP2_MOUSE | P97433 mus musculu |
| 35 | 73 | 8.0 | 61 | 1 | MTID_PIG | P79377 sus scrofa |
| 36 | 73 | 8.0 | 4393 | 1 | PGEM_HUMAN | P98160 homo sapien |
| 37 | 72.5 | 8.0 | 450 | 1 | NH14_CAEEL | O02151 caenorhabdi |
| 38 | 72.5 | 8.0 | 634 | 1 | 2147_MOUSE | O61510 mus musculu |
| 39 | 72.5 | 8.0 | 780 | 1 | PINC_HUMAN | O05209 homo sapien |
| 40 | 72.5 | 8.0 | 788 | 1 | ITB6_HUMAN | P18564 homo sapien |
| 41 | 72.5 | 8.0 | 1696 | 1 | PCK5_BRACL | O9nj15 branchiosto |
| 42 | 72 | 7.9 | 290 | 1 | XHD8_HUMAN | P13378 homo sapien |
| 43 | 72 | 7.9 | 308 | 1 | ACPI_ENTHI | P36184 entamoeba h |
| 44 | 72 | 7.9 | 354 | 1 | VEGD_HUMAN | O43915 homo sapien |
| 45 | 72 | 7.9 | 448 | 1 | EDAR_MOUSE | O9r187 mus musculu |

ALIGNMENTS

RESULT 1
ID T13X_HUMAN STANDARD; PRT; 293 AA.
AC O14836;
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane activator and CAML interactor).
GN TNFRSF13B OR TACI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RX MEDLINE=97458245; PubMed=9311921;
RA von Buelow G.-U., Bram R.U.;
RT "NF-AT activation induced by a CAML-interacting member of the tumor necrosis factor receptor superfamily.";
RL Science 278:138-141(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Straube-Blood;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP FUNCTION.
RX MEDLINE=20519647; PubMed=10956646;
RA Wu Y., Bressette D., Carrell J.A., Kaufman T., Peng P., Taylor K., Gan Y., Cho Y.H., Garcia A.D., Gollatz E., Dimke D., Lafleur D., Mlgone T.S., Nardelli B., Wei P., Ruben S.M., Ullrich S.J., Olsen H.S., Kanekaraj P., Moore P.A., Baker K.P.;
RA "Tumor necrosis factor (TNF) receptor superfamily member TACI is a high affinity receptor for TNF family members APRIL and BLyS.";
RL J. Biol. Chem. 275:35478-35485(2000).
RN [4]
RP FUNCTION.
RX MEDLINE=21170294; PubMed=10973284;
RA Yu G., Boone T., Delaney J., Hawkin N., Kelley M., Ramakrishnan M., McCabe S., Qiu W.R., Korman M., Xia X.-Z., Guo J., Scollina M., Boyle W.J., Sarsel I., Hsu H., Senaldi G., Thell L.B.;
RA "APRIL and TRAF-1 and receptors BCMA and TRAF1: system for regulating humoral immunity.";
RL Nat. Immunol. 1:252-256(2000).
RN [5]
RP FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TL1A/BAPF/BLYS that binds both ligands with similar high affinity. Mediates calcineurin-dependent activation of NF-AT, as well as activation of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-cell function and the regulation of humoral immunity.
RN [6]
RP SUBUNIT: Binds TRAF2, TRAF3 and TRAF6. Binds the NH2-terminal domain of CAML with its C-terminus.
RN [7]
RP SUBCELLULAR LOCATION: Type III membrane protein.
RN [8]
RP TISSUE SPECIFICITY: Highly expressed in spleen, thymus, small intestine and peripheral blood leukocytes. Expressed in resting B-

cells and activated T-cells, but not in resting T-cells.
 CC -1- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
 CC -1- CAUTION: It is uncertain whether Met-1 or Met-31 is the initiator.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 CC EMBL, AF023614, AAC51790.1; -
 CC EMBL, BC028072, AAH28072.1; -
 CC GenBank, HGNC:18153, TNFRSF13B.
 CC MIM: 604907; -
 CC InterPro: IPR001368; TNFR_C6.
 CC PROSITE: PS00652; TNFR_NGFR_1; 1.
 CC PROSITE: PS50050; TNFR_NGFR_2; FALSE NEG.
 CC Receptor; Immune response; Signal-anchor; Transmembrane; Glycoprotein;
 CC Repeat.
 CC DOMAIN 1 165 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 166 186 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
 CC (POTENTIAL).
 CC REPEAT 187 293 CTOPPLASMITIC (POTENTIAL).
 CC REPEAT 33 67 TNFR-CYS 1.
 CC REPEAT 70 104 TNFR-CYS 2.
 CC DISULFID 34 47 BY SIMILARITY.
 CC DISULFID 50 62 BY SIMILARITY.
 CC DISULFID 54 66 BY SIMILARITY.
 CC DISULFID 71 86 BY SIMILARITY.
 CC DISULFID 89 100 BY SIMILARITY.
 CC DISULFID 93 104 BY SIMILARITY.
 CC CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CONFLICT 251 251 P -> L (TN REF. 2).
 CC SEQUENCE 293 AA, 31816 MW, 41179933DB17A5EB CRC64;
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 CC Query Match 100.0%; Score 909; DB 1; Length 293;
 CC Best Local Similarity 100.0%; Pred. No. 4.3e-79;
 CC Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 MGLGSRGSRGSRVQDERFPGQMTGVAMSCPEEQYWDPLGTGCMCKTICNHQSOR 60
 CC Db 1 MGLGSRGSRGSRVQDERFPGQMTGVAMSCPEEQYWDPLGTGCMCKTICNHQSOR 60
 CC QY 61 TCAAFCSRSCRCRQGFYDHLRDCISGASICGQHPKQCAIFCEKXKSPVNLPEELR 120
 CC Db 61 TCAAFCSRSCRCRQGFYDHLRDCISGASICGQHPKQCAIFCEKXKSPVNLPEELR 120
 CC QY 121 QRSGEVENSNSGRYQGLEHRSSEASPALPGIKLSADQVALVYST 166
 CC Db 121 QRSGEVENSNSGRYQGLEHRSSEASPALPGIKLSADQVALVYST 166
 CC
 CC RESULT 2
 CC ID T13X MOUSE STANDARD; PRT; 249 AA.
 CC AC Q9ERT5; Q9DBZ3;
 CC DT 15-JUN-2002 (Rel. 41, Created)
 CC DT 15-JUN-2002 (Rel. 41, Last sequence update)
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
 CC DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane
 CC activator and CAML interactor).
 CC GN TNFRSF13B OR TACI.
 CC OS Mus musculus (Mouse).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC TISSUE=Spleen;
 CC RX MEDLINE=21177254; PubMed=10881172;
 CC Yan M., Mörsters S.A., Grewal I.S., Wang H., Ashkenazi A.,

RA Dixit V.M.;
 RT "Identification of a receptor for Bvys demonstrates a crucial role in
 RT humoral immunity";
 RL Nat. Immunol. 1:37-41(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamaoka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kanakawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guetlich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Saeki H., Sato K., Schoenbach C., Seye T., Shibata Y., Storch K.-P.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kontecki S.,
 RA Hayashizaki Y.;
 RL "Functional annotation of a full-length mouse cDNA collection";
 RN Nature 409:685-690(2001).
 RP FUNCTION.
 RX MEDLINE=20341628; PubMed=10880535;
 RA Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,
 RA Theill L.B., Colombero A., Solovayev I., Lee F., McCabe S., Elliott R.,
 RA Miner K., Hawkins J., Guo J., Stolina M., Yu G., Wang J., Delaney J.,
 RA Meng S.-Y., Boyle W.J., Heu H.;
 RT "TRAF1 is a TRAF-interacting receptor for TLR1-1, a tumor necrosis
 RT factor family member involved in B cell regulation";
 RL J. Exp. Med. 192:137-143(2000).
 RN [4]
 RP FUNCTION.
 RX MEDLINE=21322748; PubMed=11429548;
 RA Wang H., Mörsters S.A., Baker T., Chan B., Lee W.P., Fu L., Tumas D.,
 RA Yan M., Dixit V.M., Ashkenazi A., Grewal I.S.;
 RT "TRAF1-ligand interactions are required for T cell activation and
 RT collagen-induced arthritis in mice";
 RL Nat. Immunol. 2:632-637(2001).
 CC -1- FUNCTION: Receptor for TNFRSF13/APRIL and TNFRSF13B/BAFF/BLYS
 CC that binds both ligands with similar high affinity. Mediates
 CC calcineurin-dependent activation of NF-kappa-B, as well as activation
 CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
 CC cell function and the regulation of humoral immunity (by
 CC similarity).
 CC -1- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
 CC domain of CAMLG with its C-terminus (by similarity).
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein (probable).
 CC -1- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
 CC -----
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 CC -----
 CC EMBL, AF257673; AAC00081.1; -
 CC EMBL, AK004668; BAB33457.1; -
 CC MGD; MGI:1889411; Tnftrsf13b.
 CC PROSITE: PS00652; TNFR_NGFR_1; 1.
 CC PROSITE: PS50050; TNFR_NGFR_2; 2.
 CC Receptor; Immune response; Signal-anchor; Transmembrane; Repeat.
 CC DOMAIN 1 128
 CC TRANSMEM 129 149 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)

FT DOMAIN 150 249 (POTENTIAL).
 FT REPEAT 5 38 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 42 76 TNFR-CYS 1.
 FT DISULFID 6 19 TNFR-CYS 2.
 FT DISULFID 22 34 BY SIMILARITY.
 FT DISULFID 26 38 BY SIMILARITY.
 FT DISULFID 43 58 BY SIMILARITY.
 FT DISULFID 61 72 BY SIMILARITY.
 FT DISULFID 65 76 BY SIMILARITY.
 FT CONFLICT 137 I -> F (IN REF. 2).
 SQ SEQUENCE 249 AA: 26947 MM; CBAFF261C2931D81 CAC64;
 Query Match 46.1%; Score 419.5; DB 1; Length 249;
 Best Local Similarity 55.1%; Pred. No. 8.6e-33;
 Matches 76; Conservative 22; Mismatches 31; Indels 9; Gaps 2;

Qy 29 VAMRCEBQYVDPPLGTCMSCKTICNHSQRTCAAFCSLSCKRQCKFYTHLIDCIS 88
 Db 1 MAMAPCPDQYWDSSRKSCVSCALTCQSRQRTCTDPCFKINCRKQGRYDHLGACVS 60
 Qy 89 CASIOGHKQCAFCEKNCENKASPVNLPELARBQASGEVYNNDSNGRYOGLHRGSEASP 148
 Db 61 CDSTQHPQCAHFCERKPRSOANLQPELGRPOAGEVEVRSDNSGRQSGSHG----- 114
 Qy 149 ALPGIKLSADQVALVYST 166
 Db 115 --PGLRLSSDQLT-YCT 129

RESULT 3
 PC55 MOUSE STANDARD; PRT: 1877 AA.
 AC 004592; 062040;
 ID 01-FEB-1995 (Rel. #1, Created)
 DT 16-OCT-2001 (Rel. #0, Last sequence update)
 DT 15-JUN-2002 (Rel. #1, Last annotation update)
 DB Proprotein convertase subtilisin/kexin type 5 precursor (EC 3.4.21.-)
 DB (Proprotein convertase PCS5) (Subtilisin/kexin-like protease PCS5)
 DB (Convertase PCS5) (PC6) (Subtilisin-like proprotein convertase 6) (SEPC6).
 DE PCSK5.
 GN PCSK5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE OF 330-1877 FROM N.A. (ISOFORM PCS5).
 RC STRAIN=ICR; TISSUE=Intestine;
 RA MEDLINE=93327934; PubMed=8335106;
 RA Nakagawa T., Murakami K., Nakayama K.;
 RT "Identification of an isoform with an extremely large Cys-rich region
 of PC6, a Kex2-like processing endoprotease.";
 RL FEBS Lett. 327:165-171 (1993).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM PCSA).
 RC TISSUE=Brain, and Intestine;
 RX MEDLINE=93224489; PubMed=8468318;
 RA Nakagawa T., Hosaka M., Torii S., Watanabe T., Murakami K.,
 RA Nakayama K.;
 RT "Identification and functional expression of a new member of the
 mammalian Kex2-like processing endoprotease family: its striking
 structural similarity to PACE4.";
 RL J. Biochem. 113:132-135 (1993).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM PCSA).
 RC TISSUE=Adrenal cortex;
 RX MEDLINE=933442056; PubMed=8341687;
 RA Lussan J., Vleau D., Hamelin J., Day R., Chretien M., Seidah N.G.;
 RT "cDNA structure of the mouse and rat subtilisin/kexin-like PCS5: a
 candidate proprotein convertase expressed in endocrine and
 nonendocrine cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695 (1993).

RN [4]
 RP PARTIAL SEQUENCE, AND SUBCELLULAR LOCATION.
 RX MEDLINE=97103178; PubMed=8947550;
 RA De Bie I., Marcinkiewicz M., Malide D., Lazure C., Nakayama K.,
 RA Bandayan M., Seidah N.G.;
 RT "The isoforms of proprotein convertase PCS5 are sorted to different
 subcellular compartments.";
 RL J. Cell Biol. 135:1261-1275 (1996).
 RN [5]
 RP DEVELOPMENTAL EXPRESSION.
 RX MEDLINE=96293359; PubMed=8698813;
 RA Constam D.B., Calton M., Robertson E.J.;
 RT "SPC4, SPC6, and the novel protease SPC7 are coexpressed with bone
 morphogenetic proteins at distinct sites during embryogenesis.";
 RL J. Cell Biol. 134:181-191 (1996).
 RN [6]
 RP DEVELOPMENTAL EXPRESSION.
 RX MEDLINE=97436919; PubMed=9291583;
 RA Rancourt S.L., Rancourt D.E.;
 RT "Murine subtilisin-like proteinase SPC6 is expressed during embryonic
 implantation, somitogenesis, and skeletal formation.";
 RL Dev. Genet. 21:75-81 (1997).
 CC -1- FUNCTION: LIKELY TO REPRESENT A WIDESPREAD ENDOPEPTIDASE ACTIVITY
 WITHIN THE CONSTITUTIVE AND REGULATED SECRETORY PATHWAY. CAPABLE
 OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF. MAY BE RESPONSIBLE
 FOR THE MATURATION OF GASTROINTESTINAL PEPTIDES. MAY BE INVOLVED
 IN THE CELLULAR PROLIFERATION OF ADRENAL CORTEX VIA THE ACTIVATION
 OF GROWTH FACTORS.
 CC -1- CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR
 PROTEINAINS BY CLEAVAGE OF ARG-XAA-YAA-ARG-|-ZAA BONDS, WHERE XAA
 CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.
 CC -1- SUBCELLULAR LOCATION: PCSA IS SECRETED THROUGH THE REGULATED
 SECRETORY PATHWAY. PCSB IS A TYPE I MEMBRANE PROTEIN LOCALIZED TO
 A PARANUCLEAR POST-GOLGI NETWORK COMPARTMENT IN COMMUNICATION WITH
 EARLY ENDOSOMES.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS, PCSB/LONG (SHOWN HERE)
 AND PCSA/SHORT; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: PCSA IS EXPRESSED IN MOST TISSUES BUT IS MOST
 ABUNDANT IN THE INTESTINE AND ADRENALS. PCSB IS EXPRESSED IN THE
 INTESTINE, ADRENALS AND LUNG BUT NOT IN THE BRAIN.
 CC -1- DEVELOPMENTAL STAGE: WEAKLY EXPRESSED THROUGHOUT THE EMBRYO,
 EXCEPT IN THE DEVELOPING NERVOUS SYSTEM, THE RIBS AND THE LIVER,
 BUT MARKEDLY UPREGULATED AT DISCRETE SITES DURING DEVELOPMENT. AT
 E6.5, PROMINENT EXPRESSION OBSERVED IN DIFFERENTIATED DECIDUA. AT
 E7.5, INTENSE EXPRESSION IN EXTRAEMBRYONIC ENDODERM, AMNION AND
 NASCENT MESODERM. AT 8.5, ABUNDANT EXPRESSION IN SOMITES AND YOLK
 SAC FOLLOWED BY A CONTINUATION TO DERMATOTOME COMPARTMENT. BETWEEN
 E9.5 AND E11.5, ABUNDANT EXPRESSION IN AER (THICKENED ECTODERMAL
 CELLS OF LIMB BUDS). AT E12.5, EXPRESSION IN THE LIMBS IS CONFINED
 TO THE CONDENSING MESenchym SURROUNDING THE CARTILAGE. AT THIS
 STAGE, STRONG EXPRESSION ALSO DETECTED IN VERTEBRAL AND FACIAL
 CARTILAGE PRIMORDIA AND IN THE MUSCLE OF THE TONGUE. AT E16.5,
 ABUNDANT EXPRESSION IN EPITHELIAL CELLS OF THE INTESTINAL VILLI.
 CC -1- ISOFORM A IS MOST ABUNDANT AT ALL STAGES BUT SIGNIFICANT LEVELS OF
 ISOFORM B OCCUR AT E12.5.
 CC -1- DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE
 ASSISTING THE FOLDING OF THE ZMOGEN WITHIN THE ENDOPLASMIC
 RETICULUM.
 CC -1- DOMAIN: AC 1 AND AC 2 (CLUSTERS OF ACIDIC AMINO ACIDS) CONTAIN
 SORTING INFORMATION. AC 1 DIRECTS TGN LOCALIZATION AND INTERACTS
 WITH THE TGN SORTING PROTEIN PACS-1.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.
 CC -1- SIMILARITY: CONTAINS 1 HOWO B/P DOMAIN.
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 CC EMBL; D17583; BAA04507.1; -.

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DR EMBL: D12619; BAA02143.1; -.
DR EMBL: L14932; AAA74636.1; -.
DR PIR: JX0248; JX0248.
DR PIR: A48225; A48225.
DR HSP: G99405; IMPR.
DR MEROPS: S08_076; -.
DR MGD: MG1:97515; Peck5.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR002174; Furin-like.
DR InterPro: IPR002884; P_domain.
DR InterPro: IPR000209; Peptidase_S8.
DR Pfam: PF00082; Peptidase_S8; 1.
DR Pfam: PF01483; P; PARTIAL.
DR PRINTS: PR00723; SUBTILISIN.
DR ProDom: PD000717; P_domain; 1.
DR SMART: SM00001; EGF_1like; 2.
DR SMART: SM00261; FU_22.
DR PROSITE: PS00136; SUBTILASE_ASP; 1.
DR PROSITE: PS00137; SUBTILASE_HIS; 1.
DR PROSITE: PS00138; SUBTILASE_SER; 1.
DR Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal;
KM Cleavage on pair of basic residues; Repeat; Alternative splicing;
KW Transmembrane.
FT SIGNAL 1 34
FT PROPEP 35 116
FT CHAIN 117 1877
FT
FT DOMAIN 117 1768 PROTEIN CONVERTASE SUBTILISIN/KEXIN
FT TRASMEN 1769 1789 TYPE 5.
FT DOMAIN 1790 1877 POTENTIAL.
FT DOMAIN 117 452 CTOPLASTIC (POTENTIAL).
FT DOMAIN 464 602 CATALYTIC.
FT DOMAIN 638 1753 HOMO B.
FT DOMAIN 1825 1844 CYS-RICH MOTIF (CRM) REGION.
FT DOMAIN 1856 1877 AC 1.
FT SITE 116 117 AC 2.
FT SITE 521 523 CLEAVAGE (AUTO-) (BY SIMILARITY).
FT ACT SITE 173 523 CELL ATTACHMENT SITE (POTENTIAL).
FT ACT SITE 214 214 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT SITE 388 388 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CAROXYD 227 227 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROXYD 383 383 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROXYD 667 667 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROXYD 754 754 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROXYD 804 804 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROXYD 854 854 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROXYD 951 951 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROXYD 1016 1016 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROXYD 1220 1220 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROXYD 1317 1317 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROXYD 1523 1523 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROXYD 1711 1711 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROXYD 1733 1733 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 878 915 GEYIDQGHCTCEASCKAKPTEDCISCVTVLD ->
FT VARSPLIC 878 915 ATEESWAEGLFMTLVKKNLCORXVLOQCCTCTFOG
FT VARSPLIC 878 915 (IN ISOFORM PCSA).
FT VARSPLIC 878 915 MISSING (IN ISOFORM PCSA).
SQ SEQUENCE 1877 AA; 209287 MW; EC850E2DF20EALIC3 CRC64;

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Query Match 10.7%; Score 97.5; DB 1; Length 1877;
 Best Local Similarity 30.2%; Pred. No. 0.21;
 Matches 29; Conservative 12; Mismatches 32; Indels 23; Gaps 7;

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QY 14 RYDQ--EEFPGQIMTVAMRSGPREQYWDPLG-TCMSCKITCN-----HSGRCARAF 65
DB 956 RADKIGQGEF---LYHGELENCVPGHY--PAKGHTCLCPDNCCLCYNPHICSRMSGY 1010
QY 66 -----CRSLSCRKQGGKPYDHLRLDCLSCASIC 93
DB 1011 VLIIPNHTQCKLECR--QGEFQDSFEYECMPCBEGC 1044

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RESULT 4
ID Y2A CAEEL STANDARD; PRT; 867 AA.
AC P34447; P34448;
DT 01-FEB-1994 (Rel. 28, Created)
DT 15-UN-2002 (Rel. 41, Last sequence update)
DT 15-UN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein F54F2.2 in chromosome III, isoform a.
GN F54F2.2/F54F2.3/F54F2.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OK NCBI_taxid=6239;
RP [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ahncough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rinken L., Roopra A., Saunders D., Showkeen R.,
RA Sims M., Smaildon N., Smith A., Smith M., Sonnenhammer B., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Woldman P.;
RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Nature 368:32-38(1994).
RP [2]
RP REVISIONS, AND ALTERNATIVE SPLICING.
RA Waterson R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; a (shown here) and b (AC
CC -1- SIMILARITY: CONTAINS 2 PHD ZINC-FINGER DOMAINS.
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CC EMBL: U23645; AAC26137.1; -.
DR PIR: S44827; S44827.
DR WormPep: F54F2.2a; CE25003.
DR InterPro: IPR001965; Znf_PHD.
DR Pfam: PF00628; PHD; 1.
DR SMART: SM00249; PHD; 2.
KW Hypothetical protein; Metal-binding; Zinc; Zinc-finger; Repeat;
KW DNA-binding; Nuclear protein; Alternative splicing.
FT ZN FING 5 57 PHD-TYPE 1.
FT ZN FING 124 185 PHD-TYPE 2.
SQ SEQUENCE 867 AA; 92189 MW; 7B582DC2529CFEAD CRC64;

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Query Match 9.8%; Score 89; DB 1; Length 867;
 Best Local Similarity 32.5%; Pred. No. 0.61;
 Matches 27; Conservative 8; Mismatches 28; Indels 20; Gaps 5;

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QY 34 PREQYMPPLIGTQSC-KTICNHSORTCAFCRSLSCKEOKFYDHLRLDCLSCASI 92
DB 130 CNEEPNPAKKGACSCSKSTCKRSFHYTCAQ-RKGLLC--EEGAI----- 172
QY 93 CGQPKQCAVFCENTLRSPVNL 115
DB 173 -SRNVKTCGY-CENHLKRAINDP 193

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RESULT 5
XEDA HUMAN STANDARD; PRT; 297 AA.
ID XEDA HUMAN
AC O9H4V5;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member XEDAR (X-linked
GN XEDAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. AND MUTAGENESIS OF GLU-256.
RC TISSUE=Fetal kidney;
RX MEDLINE=20495245; PubMed=11039935;
RA Yan M., Wang L.-C., Hymowitz S.G., Schilbach S., Lee J., Goddard A.,
RA de Vos A.M., Gao W.-Q., Dixit V.M.;
RT "Two-amino acid molecular switch in an epithelial morphogen that
RT regulates binding to two distinct receptors.";
RL Science 290:523-527(2000).
CC -1- FUNCTION: Receptor for EDA isoform A2, but not for EDA isoform
CC A1. Mediates the activation of NF-kappa-B. Activation seems to
CC be mediated by binding to TRAF6.
CC -1- SUBUNIT: Associates with TRAF1, TRAF3 and TRAF6.
CC -1- SUBCELLULAR LOCATION: Type III membrane protein.
CC -1- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC -----
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CC -----
DR EMBL; AF298812; AAC28761.1; -
DR MIM; 300276; -
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
KW Receptor; Developmental protein; Differentiation; Transmembrane;
KW Glycoprotein; Repeat.
FT DOMAIN 1 138 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 139 159 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
FT FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 160 297
FT REPEAT 2 41 TNFR-CYS 1.
FT REPEAT 43 83 TNFR-CYS 2.
FT REPEAT 85 118 TNFR-CYS 3.
FT DISULFID 3 15 BY SIMILARITY.
FT DISULFID 18 31 BY SIMILARITY.
FT DISULFID 21 41 BY SIMILARITY.
FT DISULFID 44 58 BY SIMILARITY.
FT DISULFID 61 75 BY SIMILARITY.
FT DISULFID 64 83 BY SIMILARITY.
FT DISULFID 86 104 BY SIMILARITY.
FT DISULFID 107 118 BY SIMILARITY.
FT CARBOHYD 74 74 N-LINKED (GLCNAC... ) (POTENTIAL).
FT MUTAGEN 256 E->R; ABOLISHES TRAF6 ASSOCIATION.
SQ SEQUENCE 297 AA; 32728 MW; 0E71127C6C48240C CRC64;

Query Match 9.5%; Score 86; DB 1; Length 297;
Best Local Similarity 22.0%; Pred. No. 0.4;
Matches 26; Conservative 19; Mismatches 31; Indels 42; Gaps 7;

Cy 34 CPEBOYMDPLTGMCKTIC--NHOSORTCA-----AFGSLSRKKGKGFYHLRLD 85
Db 3 COENEYWDQ-WGRPYTCOR-CGPQGLSRDCGSGGGDAYCTACPPRRYKSSWGHRCOS 60
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86 CISCA-----SICGHPKQCAVFCENKLSFVNPPLPRRORSSEVEN 128
Cy 61 CITCAVIRVQKNCTATSNVACGD-----C-----LPRFRKTRIGGLQD 101
Db 61 CITCAVIRVQKNCTATSNVACGD-----C-----LPRFRKTRIGGLQD 101

RESULT 6
RECK MOUSE STANDARD; PRT; 971 AA.
ID RECK MOUSE
AC Q920J1;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Reversion-inducing cysteine-rich protein with Kazal motifs precursor
GN RECK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99007295; PubMed=9789069;
RA Takahashi C., Sheng Z., Horan T.P., Kitayama H., Maki M., Hitomi K.,
RA Kitaura Y., Takai S., Sasahara R.M., Horimoto A., Ikawa Y.,
RA Ratzkin B.J., Arakawa T., Noda M.;
RT "Regulation of matrix metalloproteinase-9 and inhibition of tumor
RT invasion by the membrane-anchored glycoprotein RECK.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:13221-13226(1998).
CC -1- FUNCTION: Negatively regulates matrix metalloproteinase-9 (MMP-9)
CC by suppressing MMP-9 secretion, and by direct inhibition of its
CC enzymatic activity. RECK down-regulation by oncogenic signals may
CC facilitate tumor invasion and metastasis. Appears to also
CC regulate MMP-2 and MT1-MMP, which are involved in cancer
CC progression (By similarity).
CC -1- SUBUNIT: Interacts with MMP-9.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC expressed in mesenchymal tissues and is relatively abundant in the
CC marginal zone of the neural tube and large blood vessels such as
CC the aorta.
CC -1- SIMILARITY: CONTAINS 3 KAZAL-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL; AB006960; BAA34061.1; -
DR MGD; MGI:1855698; Reck.
DR InterPro; IPR002350; Kazal.
DR Pfam; PF00050; Kazal; 2.
DR SMART; SM00280; KAZAL; 2.
DR PROSITE; PS00282; KAZAL; 1.
KW Signal; Glycoprotein; GPI-anchor; Serine protease inhibitor;
KW Membrane; Anti-oncogene; Repeat.
FT SIGNAL 1 22
FT CHAIN 23 942
FT PROPEP 943 971
FT LIPID 942 942 GPI-ANCHOR (POTENTIAL).
FT DOMAIN 633 677 KAZAL-LIKE 1.
FT DOMAIN 704 750 KAZAL-LIKE 2 (DEGENERATE).
FT DOMAIN 751 787 KAZAL-LIKE 3 (DEGENERATE).
FT DOMAIN 37 338 5 X KNOT REPEATS.
FT REPEAT 37 84 KNOT 1.
FT REPEAT 104 141 KNOT 2.
FT REPEAT 151 197 KNOT 3.
FT REPEAT 216 263 KNOT 4.
FT REPEAT 292 338 KNOT 5.
```



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FT DISULFID 635 654 BY SIMILARITY.
FT DISULFID 633 658 BY SIMILARITY.
FT DISULFID 633 658 BY SIMILARITY.
FT CARBOHYD 39 39 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 971 AA, 106134 MW, 2FC8EBE38A20F86D CRC64,
  9.1%; Score 83; DB 1; Length 971;
  Beef Local Similarity 22.4%; Pred. No. 2.5;
  Matches 33; Conservative 16; Mismatches 42; Indels 56; Gaps 8;
  34 CPEE-QYMDPL-----LGTG-----MSCRTICNHQSQRTCAFCRSLS 70
  74 CPETWEIWSNMSNSLPGVFKSKDGNVGGCCCLALGLEBRQACXKASKNDI----SKY 129
  71 CRKQCKFDHLRLDCIS-----CASTCGQHPKOCANFCENKLRSPVNLPELRQRS 123
  130 CRKE-----YENALFSCISINEMGVSVCYAGHH-TWCRFCQAFRT----- 171
  124 GEVENSDNSGRYQGLEHRSSEAPAL 150
  172 ----DSSPGSPQIKAVENYCASISPOL 194
  Db
  7
  RESULT 7
  APNU_PIG STANDARD; PRT; 1150 AA.
  ID APNU_PIG STANDARD; PRT; 1150 AA.
  AC P12021;
  DT 01-OCT-1989 (Rel. 12, Created)
  DT 01-DEC-1992 (Rel. 24, Last sequence update)
  DT 15-JUN-2002 (Rel. 41, Last annotation update)
  DE Apomucin (Mucin core protein) (Fragment).
  OS Suis scrofa (Pig).
  OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
  NC NCBI_TaxID:9823;
  RN [1]
  RP SEQUENCE FROM N.A.
  RC TISSUE=Submaxillary gland;
  RA Eckhardt A.E., Timpte C.S., Abernethy J.L., Zhao Y., Hill R.L.;
  RT "Porcine submaxillary mucin contains a cysteine-rich,
  RT carboxyl-terminal domain in addition to a highly repetitive,
  RT glycosylated domain";
  RL J. Biol. Chem. 266:9678-9686(1991).
  RN [2]
  RP SEQUENCE OF 1-503 FROM N.A.
  RC TISSUE=Submaxillary gland;
  RA MEDLINE=91236743; PubMed=2033060;
  RA Timpte C.S., Eckhardt A.E., Abernethy J.L., Hill R.L.;
  RT "Porcine submaxillary mucin contains a cysteine-rich,
  RT identical sequences of 81 residues";
  RL J. Biol. Chem. 263:1081-1088(1988).
  RN [3]
  RP SEQUENCE OF 45-80.
  RC TISSUE=Submaxillary gland;
  RA MEDLINE=87280230; PubMed=3611111;
  RA Eckhardt A.E., Timpte C.S., Abernethy J.L., Toumadje A.,
  RA Johnson W.C. Jr., Hill R.L.;
  RT "Structural properties of porcine submaxillary gland apomucin";
  RL J. Biol. Chem. 262:11339-11344(1987).
  RN [4]
  RP CARBOHYDRATE-LINKAGE SITES, AND SEQUENCE OF 45-125.
  RC TISSUE=Submaxillary gland;
  RA MEDLINE=97248516; PubMed=9092502;
  RA Getzen T.A., Owens C.L., Pasumathy M.;
  RT "Determination of the site-specific O-glycosylation pattern of the
  RT porcine submaxillary mucin tandem repeat glycopeptide. Model proposed
  RT for the polypeptide:galnac transferase peptide binding site.";
  RL J. Biol. Chem. 272:9709-9719(1997).

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CC - FUNCTION: APOMUCIN IS PART OF MUCIN, THE MAJOR GLYCOPROTEIN
CC SYNTHESIZED AND SECRETED BY MUCOUS CELLS OF THE SUBMAXILLARY
CC GLAND. ITS HIGHLY VISCOUS AQUEOUS SOLUTIONS SERVE TO LUBRICATE
CC THE ORAL CAVITY AND TO PROTECT IT FROM THE EXTERNAL
CC ENVIRONMENT.
CC - SUBUNIT: INTERMOLECULAR DISULFIDE BONDS COULD HELP MAINTAIN A
CC MULTIMERIC MUCIN STRUCTURE.
CC - SUBCELLULAR LOCATION: Secreted.
CC - TISSUE SPECIFICITY: SUBMAXILLARY MUCOSAE.
CC - DOMAIN: CONTAINS TANDEMLY REPEATED, IDENTICAL SEQUENCES OF 81
CC RESIDUES.
CC - PTM: EXTENSIVELY O-LINKED GLYCOSYLATED ON SER AND THR RESIDUES OF
CC THE REPEAT UNITS. HIGHEST GLYCOSYLATION APPEARS TO OCCUR ON SER
CC RESIDUES WHICH HAVE GLY AT POSITIONS AT +2 OR -2 FROM THE
CC GLYCOSYLATION SITE OR, WHERE GLY IS THE PENULTIMATE RESIDUE, THE
CC PRESENCE OF PROLINE (USUALLY AT POSITION +3 OR -3) APPEARS TO ALSO
CC ENHANCE GLYCOSYLATION.
CC - SIMILARITY: CONTAINS 1 WFRC DOMAIN.
CC - SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE (CTCK) DOMAIN.
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL, M61883; AAA30998.1; -.
CC EMBL, M21174; AAA30990.1; -.
CC PIR, A40009; A40009.
CC InterPro; IPR000359; Cys_knot.
CC InterPro; IPR01007; WFRC.
CC Pfam; PF00007; Cys_knot; 1.
CC SMART; SMO0214; WFC; 1.
CC PROSITE; PS01185; CTCK_1; 1.
CC PROSITE; PS01225; CTCK_2; 1.
CC DR PROSITE; PS01208; WFRC; 1.
CC DR Glycoprotein; Repeat.
CC KM NON TER 1 368 81 AA TANDEM REPEATS.
CC FT DOMAIN <1 44 1.
CC FT REPEAT <1 44 1.
CC FT REPEAT 45 125 2.
CC FT REPEAT 126 206 3.
CC FT REPEAT 207 287 4.
CC FT REPEAT 288 368 5.
CC FT REPEAT 369 391 6 (INCOMPLETE).
CC FT DOMAIN 929 995 WFRC.
CC FT DOMAIN 1062 1146 CTCK.
CC FT DISULFID 1062 1109 BY SIMILARITY.
CC FT DISULFID 1076 1123 BY SIMILARITY.
CC FT DISULFID 1085 1139 BY SIMILARITY.
CC FT DISULFID 1089 1141 BY SIMILARITY.
CC FT DISULFID ? 1145 BY SIMILARITY.
CC FT CARBOHYD 46 46 O-LINKED (GALNAC. . .) (MUCIN TYPE).
CC FT CARBOHYD 50 50 O-LINKED (GALNAC. . .) (MUCIN TYPE).
CC FT CARBOHYD 51 51 O-LINKED (GALNAC. . .) (MUCIN TYPE).
CC FT CARBOHYD 57 57 O-LINKED (GALNAC. . .) (MUCIN TYPE).
CC FT CARBOHYD 58 58 O-LINKED (GALNAC. . .) (MUCIN TYPE).
CC FT CARBOHYD 61 61 O-LINKED (GALNAC. . .) (MUCIN TYPE).
CC FT CARBOHYD 66 66 O-LINKED (GALNAC. . .) (MUCIN TYPE).
CC FT CARBOHYD 67 67 O-LINKED (GALNAC. . .) (MUCIN TYPE).
CC FT CARBOHYD 73 73 O-LINKED (GALNAC. . .) (MUCIN TYPE).
CC FT CARBOHYD 74 74 O-LINKED (GALNAC. . .) (MUCIN TYPE).
CC FT CARBOHYD 76 76 O-LINKED (GALNAC. . .) (MUCIN TYPE).
CC FT CARBOHYD 77 77 O-LINKED (GALNAC. . .) (MUCIN TYPE).
CC FT CARBOHYD 81 81 O-LINKED (GALNAC. . .) (MUCIN TYPE).
CC FT CARBOHYD 83 83 O-LINKED (GALNAC. . .) (MUCIN TYPE).
CC FT CARBOHYD 87 87 O-LINKED (GALNAC. . .) (MUCIN TYPE).
CC FT CARBOHYD 91 91 O-LINKED (GALNAC. . .) (MUCIN TYPE).
CC FT CARBOHYD 93 93 O-LINKED (GALNAC. . .) (MUCIN TYPE).
CC FT CARBOHYD 94 94 O-LINKED (GALNAC. . .) (MUCIN TYPE).

```


Db 772 --EDGRRFNG--ODCPCHRFCAFCAGAGADGCTGCTGEMED 811

RESULT 9

LRP2_RAT ID_LRP2_RAT STANDARD; PRT; 4660 AA.

AC P98158; 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Low-density lipoprotein receptor-related protein 2 precursor (Megalyn)

DE (Glycoprotein 330).

GN LRP2.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxId=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley; TISSUE=Kidney;

RX MEDLINE=95024033; PubMed=7937880;

RA Saito A., Pietromonaco S., Loo A.K.C., Farquhar M.G.;

RT "Complete cloning and sequencing of rat gp330/'megalin,' a distinctive member of the low density lipoprotein receptor gene family.";

RT Proc. Natl. Acad. Sci. U.S.A. 91:9725-9729(1994).

RL [2]

RN FUNCTION.

RP MEDLINE=95386696; PubMed=7544804;

RA Moestrup S.K., Cui S., Vorum H., Bregengaard C., Bjorn S.E., Norris K., Gilemann U., Christensen E.I.;

RT "Evidence that epithelial glycoprotein 330/megalin mediates uptake of polybasic drugs.";

RL J. Clin. Invest. 96:1404-1413(1995).

RN [3]

RP TISSUE SPECIFICITY.

RX MEDLINE=94172242; PubMed=7510321;

RA Zheng G., Bachlueky R.R., Stamenkovic I., Strickland D.K., Brown D., Andres G., McCluskey R.T.;

RT "Organ distribution in rats of the low-density lipoprotein receptor gene family, gp330 and LRP/alpha 2MR, and the receptor-associated protein (RAP).";

RT J. Biochem. 121:531-542(1994).

CC -1- FUNCTION: BINDS PLASMINOGEN, EXTRACELLULAR MATRIX COMPONENTS, COMPLEX, APOLOPROTEIN B-ENRICHED BETA-VLDL, LIPOPROTEIN LIPASE, LACTOPERRIN, CLUSTERIN AND CALCIUM.

CC -1- FUNCTION: RECEPTOR-MEDIATED UPTAKE OF POLYBASIC DRUGS SUCH AS APROTININ, AMINOGLYCOSIDES AND POLYMYXIN B.

CC -1- SUBUNIT: FORMS A MULTIMERIC COMPLEX TOGETHER WITH A RECEPTOR-ASSOCIATED PROTEIN (RAP).

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXPRESSED IN CLATHRIN-COATED PITTS. A SOLUBLE FORM IS POSSIBLY DERIVED BY CLEAVAGE AT THE CELL SURFACE.

CC -1- TISSUE SPECIFICITY: EPITHELIAL CELLS OF KIDNEY GLOMERULUS AND PROXIMAL TUBULE, LUNG, EPIDIDYMIS, YOLK SAC, AMONG OTHERS.

CC -1- SIMILARITY: CONTAINS 36 LDL-RECEPTOR CLASS A DOMAINS.

CC -1- SIMILARITY: CONTAINS 37 LDL-RECEPTOR CLASS B DOMAINS.

CC -1- SIMILARITY: CONTAINS 17 EGF-LIKE DOMAINS.

CC -----

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CC -----

DR EMBL; L34049; AAA5369.1; -.

DR HSSP; Q07954; 1CR8.

DR GlycoSiteDB; P98158; -.

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR002172; LDL_recept A.

DR InterPro; IPR000033; ldl_receptor_rep.

DR Pfam; PF00057; ldl_recept_a; 36.

DR Pfam; PF00058; ldl_recept_b; 33.

DR PRINTS; PR00261; LDLRECEPTOR.

DR SMART; SM00179; EGF_CA; 3.

DR SMART; SM00001; EGF_like; 15.

DR SMART; SM00192; LDLA; 36.

DR SMART; SM00135; LY; 35.

DR PROSITE; PS00010; ASX_HYDROXYL; 4.

DR PROSITE; PS00022; EGF_1; 1.

DR PROSITE; PS01186; EGF_2; 8.

DR PROSITE; PS01187; EGF_CA; 3.

DR PROSITE; PS01209; LDLRA_1; 31.

DR PROSITE; PS00068; LDLRA_2; 36.

KW Glycoprotein; Repeat; Endocytosis; Coated pits; Transmembrane; Receptor; EGF-like domain; SH3-binding; Signal.

KM POTENTIAL.

FT SIGNAL 1 25

FT CHAIN 26 4660

FT FT

FT DOMAIN 26 4425

FT TRANSMEM 4426 4446

FT 4447 4660

FT DOMAIN 26 64

FT DOMAIN 65 105

FT DOMAIN 106 144

FT DOMAIN 145 181

FT DOMAIN 181 219

FT DOMAIN 220 258

FT DOMAIN 263 307

FT DOMAIN 308 346

FT DOMAIN 347 385

FT DOMAIN 435 476

FT DOMAIN 478 519

FT DOMAIN 521 566

FT DOMAIN 568 611

FT DOMAIN 612 652

FT DOMAIN 658 704

FT DOMAIN 752 793

FT DOMAIN 837 879

FT DOMAIN 881 923

FT DOMAIN 969 1013

FT DOMAIN 1023 1061

FT DOMAIN 1064 1103

FT DOMAIN 1108 1146

FT DOMAIN 1148 1186

FT DOMAIN 1186 1225

FT DOMAIN 1229 1269

FT DOMAIN 1270 1308

FT DOMAIN 1311 1351

FT DOMAIN 1350 1390

FT DOMAIN 1391 1430

FT DOMAIN 1479 1520

FT DOMAIN 1522 1563

FT DOMAIN 1567 1609

FT DOMAIN 1611 1654

FT DOMAIN 1656 1696

FT DOMAIN 1701 1742

FT DOMAIN 1791 1832

FT DOMAIN 1834 1882

FT DOMAIN 1884 1930

FT DOMAIN 1932 1972

FT DOMAIN 1973 2013

FT DOMAIN 2019 2060

FT DOMAIN 2158 2201

FT DOMAIN 2203 2245

FT DOMAIN 2247 2289

FT DOMAIN 2291 2332

FT DOMAIN 2343 2384

FT DOMAIN 2432 2477

FT FT

FT LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 2.

FT EXTRACELLULAR (POTENTIAL).

FT POTENTIAL.

FT CYTOPLASMIC (POTENTIAL).

FT LDL-RECEPTOR CLASS A 1.

FT LDL-RECEPTOR CLASS A 2.

FT LDL-RECEPTOR CLASS A 3.

FT LDL-RECEPTOR CLASS A 4.

FT LDL-RECEPTOR CLASS A 5.

FT LDL-RECEPTOR CLASS A 6.

FT LDL-RECEPTOR CLASS A 7.

FT EGF-LIKE 1.

FT EGF-LIKE 2.

FT LDL-RECEPTOR CLASS B 1.

FT LDL-RECEPTOR CLASS B 2.

FT LDL-RECEPTOR CLASS B 3.

FT LDL-RECEPTOR CLASS B 4.

FT LDL-RECEPTOR CLASS B 5.

FT EGF-LIKE 3.

FT LDL-RECEPTOR CLASS B 6.

FT LDL-RECEPTOR CLASS B 7.

FT LDL-RECEPTOR CLASS B 8.

FT LDL-RECEPTOR CLASS B 9.

FT EGF-LIKE 4.

FT LDL-RECEPTOR CLASS A 8.

FT LDL-RECEPTOR CLASS A 9.

FT LDL-RECEPTOR CLASS A 10.

FT LDL-RECEPTOR CLASS A 11.

FT LDL-RECEPTOR CLASS A 12.

FT LDL-RECEPTOR CLASS A 13.

FT LDL-RECEPTOR CLASS A 14.

FT LDL-RECEPTOR CLASS A 15.

FT EGF-LIKE 5.

FT EGF-LIKE 6.

FT CALCIUM-BINDING (POTENTIAL).

FT LDL-RECEPTOR CLASS B 10.

FT LDL-RECEPTOR CLASS B 11.

FT LDL-RECEPTOR CLASS B 12.

FT LDL-RECEPTOR CLASS B 13.

FT LDL-RECEPTOR CLASS B 14.

FT EGF-LIKE 7.

FT LDL-RECEPTOR CLASS B 15.

FT LDL-RECEPTOR CLASS B 16.

FT LDL-RECEPTOR CLASS B 17.

FT LDL-RECEPTOR CLASS B 18.

FT LDL-RECEPTOR CLASS B 19.

FT EGF-LIKE 8.

FT LDL-RECEPTOR CLASS B 20.

FT LDL-RECEPTOR CLASS B 21.

FT LDL-RECEPTOR CLASS B 22.

FT LDL-RECEPTOR CLASS B 23.

FT LDL-RECEPTOR CLASS B 24.

FT EGF-LIKE 9.

FT LDL-RECEPTOR CLASS B 25.

| | | | | |
|----|----------|------|------|-----------------------------------|
| FT | DOMAIN | 2479 | 2518 | LDL-RECEPTOR CLASS B 26. |
| FT | DOMAIN | 2520 | 2562 | LDL-RECEPTOR CLASS B 27. |
| FT | DOMAIN | 2564 | 2604 | LDL-RECEPTOR CLASS B 28. |
| FT | DOMAIN | 2605 | 2647 | LDL-RECEPTOR CLASS B 29. |
| FT | DOMAIN | 2652 | 2694 | EGF-LIKE 10. |
| FT | DOMAIN | 2699 | 2739 | LDL-RECEPTOR CLASS A 16. |
| FT | DOMAIN | 2740 | 2778 | LDL-RECEPTOR CLASS A 17. |
| FT | DOMAIN | 2779 | 2820 | LDL-RECEPTOR CLASS A 18. |
| FT | DOMAIN | 2821 | 2862 | LDL-RECEPTOR CLASS A 19. |
| FT | DOMAIN | 2863 | 2903 | LDL-RECEPTOR CLASS A 20. |
| FT | DOMAIN | 2906 | 2947 | LDL-RECEPTOR CLASS A 21. |
| FT | DOMAIN | 2948 | 2992 | LDL-RECEPTOR CLASS A 22. |
| FT | DOMAIN | 2993 | 3031 | LDL-RECEPTOR CLASS A 23. |
| FT | DOMAIN | 3032 | 3072 | LDL-RECEPTOR CLASS A 24. |
| FT | DOMAIN | 3075 | 3112 | LDL-RECEPTOR CLASS A 25. |
| FT | DOMAIN | 3113 | 3153 | EGF-LIKE 11. |
| FT | DOMAIN | 3154 | 3194 | EGF-LIKE 12. |
| FT | DOMAIN | 3241 | 3282 | LDL-RECEPTOR CLASS B 30. |
| FT | DOMAIN | 3284 | 3333 | LDL-RECEPTOR CLASS B 31. |
| FT | DOMAIN | 3335 | 3377 | LDL-RECEPTOR CLASS B 32. |
| FT | DOMAIN | 3379 | 3420 | LDL-RECEPTOR CLASS B 33. |
| FT | DOMAIN | 3421 | 3461 | LDL-RECEPTOR CLASS B 34. |
| FT | DOMAIN | 3467 | 3511 | EGF-LIKE 13. |
| FT | DOMAIN | 3512 | 3552 | LDL-RECEPTOR CLASS A 26. |
| FT | DOMAIN | 3553 | 3593 | LDL-RECEPTOR CLASS A 27. |
| FT | DOMAIN | 3594 | 3634 | LDL-RECEPTOR CLASS A 28. |
| FT | DOMAIN | 3635 | 3675 | LDL-RECEPTOR CLASS A 29. |
| FT | DOMAIN | 3678 | 3718 | LDL-RECEPTOR CLASS A 30. |
| FT | DOMAIN | 3719 | 3759 | LDL-RECEPTOR CLASS A 31. |
| FT | DOMAIN | 3759 | 3797 | LDL-RECEPTOR CLASS A 32. |
| FT | DOMAIN | 3798 | 3836 | LDL-RECEPTOR CLASS A 33. |
| FT | DOMAIN | 3842 | 3882 | LDL-RECEPTOR CLASS A 34. |
| FT | DOMAIN | 3883 | 3924 | LDL-RECEPTOR CLASS A 35. |
| FT | DOMAIN | 3928 | 3966 | LDL-RECEPTOR CLASS A 36. |
| FT | DOMAIN | 3968 | 4008 | EGF-LIKE 14. |
| FT | DOMAIN | 4009 | 4050 | EGF-LIKE 15. |
| FT | DOMAIN | 4156 | 4197 | LDL-RECEPTOR CLASS B 35. |
| FT | DOMAIN | 4199 | 4241 | LDL-RECEPTOR CLASS B 36. |
| FT | DOMAIN | 4244 | 4284 | LDL-RECEPTOR CLASS B 37. |
| FT | DOMAIN | 4332 | 4370 | EGF-LIKE 16. |
| FT | DOMAIN | 4379 | 4413 | EGF-LIKE 17. |
| FT | SITE | 4454 | 4460 | SH3-BINDING (POTENTIAL). |
| FT | SITE | 4457 | 4463 | SH3-BINDING (POTENTIAL). |
| FT | SITE | 4606 | 4609 | SH2-BINDING (POTENTIAL). |
| FT | SITE | 4619 | 4625 | SH3-BINDING (POTENTIAL). |
| FT | SITE | 4624 | 4630 | SH3-BINDING (POTENTIAL). |
| FT | SITE | 1743 | 1745 | CELL ATTACHMENT SITE (POTENTIAL). |
| FT | SITE | 4522 | 4527 | ENDOCYTOSIS SIGNAL (POTENTIAL). |
| FT | SITE | 4601 | 4606 | ENDOCYTOSIS SIGNAL (POTENTIAL). |
| FT | DISULFID | 28 | 40 | BY SIMILARITY. |
| FT | DISULFID | 35 | 53 | BY SIMILARITY. |
| FT | DISULFID | 47 | 62 | BY SIMILARITY. |
| FT | DISULFID | 67 | 80 | BY SIMILARITY. |
| FT | DISULFID | 74 | 93 | BY SIMILARITY. |
| FT | DISULFID | 87 | 103 | BY SIMILARITY. |
| FT | DISULFID | 108 | 120 | BY SIMILARITY. |
| FT | DISULFID | 115 | 133 | BY SIMILARITY. |
| FT | DISULFID | 127 | 142 | BY SIMILARITY. |
| FT | DISULFID | 147 | 157 | BY SIMILARITY. |

| Query Match | Similarity | 9.0% | Pred. No. 15 | Length 4660 |
|-------------|---|-----------------------------|---------------|-------------|
| Best Local | Conservative | 25.8% | Mismatches 64 | Indels 36 |
| Matches | 40 | 15 | 8 | Gaps |
| QY 33 | SCPEQY-WDPLTGCMSCKTICNHO--- | SQRTCAFCRSLSCKRQKGFYDH----- | 81 | |
| | | | | |
| Db 3076 | TCPPLQPRCDN--GHCIEKGRVCNHYDSDSDSGCINECLDSSISRCCHNCTDTTT | | 3133 | |
| QY 82 | -----LIRQISCAST--CGQHPKOCAYFCCENTLRSPV--NLPELRRRSGEYE | | 127 | |
| | | | | |
| Db 3134 | SPYCSGLPEYKLMSDKRSQVDIDDECKESQQLSQRKCEENVVGSYICNCAQGYIREPDKSC | | 3193 | |
| QY 128 | NNSDN-----SGRY--QGLEHRSGEASPALPGL | | 153 | |

| Db | 3194 | RÖNSNIEPYLIPSNRYIRNLTTGGSSVSLIÖG | 3228 |
|--------|--|----------------------------------|--------------|
| RESULT | 10 | | |
| RECK | HUMAN | | |
| ID | RECK_HUMAN | STANDARD; | PRI; 971 AA. |
| AC | O95980; Q8WX37; | | |
| DT | 15-JUN-2002 (Rel. 41, Created) | | |
| DT | 15-JUN-2002 (Rel. 41, Last sequence update) | | |
| DT | 15-JUN-2002 (Rel. 41, Last annotation update) | | |
| DE | Reversion-inducing cysteine-rich protein with Kazal motifs precursor (hRECK) (Suppressor of tumorigenicity 15) (ST15). | | |
| GN | Homo sapiens (Human). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. | | |
| OX | NCBI_TaxID=9606; | | |
| RP | SEQUENCE FROM N.A., AND N-GLYCOSYLATION. | | |
| RF | TISSUE= Fibroblast; | | |
| RC | MEDLINE=99007295; PubMed=9789069; | | |
| RX | Takahashi C., Sheng Z., Horan T.P., Kitayama H., Makl M., Hitomi K., Kitahara Y., Takai S., Sasahara R.M., Hozimoto A., Ikawa Y., Ratzkin B.J., Atakawa T., Noda M.; | | |
| RA | "Regulation of matrix metalloproteinase-9 and inhibition of tumor invasion by the membrane-anchored glycoprotein RECK." | | |
| RT | Proc. Natl. Acad. Sci. U.S.A. 95:13321-13326(1998). | | |
| RN | [2] | | |
| RP | SEQUENCE OF 363-971 FROM N.A. | | |
| RA | Kimberley A., | | |
| CC | Submitted (DCC-2001) to the EMBL/GenBank/DDBJ databases. | | |
| CC | -1- FUNCTION: Negatively regulates matrix metalloproteinase-9 (MMP-9) by suppressing MMP-9 secretion and by direct inhibition of its enzymatic activity. RECK down-regulation by oncogenic signals may facilitate tumor invasion and metastasis. Appears to also regulate MMP-2 and MT1-MMP, which are involved in cancer progression. | | |
| CC | -1- SUBUNIT: Interacts with MMP-9. | | |
| CC | -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor. | | |
| CC | -1- TISSUE SPECIFICITY: Expressed in various tissues and undifferentiated cells. It is undetectable in tumor-derived cell lines and oncogenically transformed cells. | | |
| CC | -1- SIMILARITY: CONTAINS 3 KAZAL-LIKE DOMAINS. | | |
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| CC | ----- | | |
| DR | EMBL; D50406; BAA34060.1; -. | | |
| DR | EMBL; AL158830; CAD13384.1; -. | | |
| DR | Genew; HGNC:11345; RECK. | | |
| DR | MIM; 605227; -. | | |
| DR | HSSP; P80424; IAN1. | | |
| DR | InterPro; IPR002350; kazal. | | |
| DR | SMART; SMO0280; KAZAL; 3. | | |
| DR | SMART; SMO0011; VMC_def; 1. | | |
| DR | PROSITE; PS00282; KAZAL; 1. | | |
| KW | Signal; Glycoprotein; GPI-anchor; Serine protease inhibitor; Membrane; Anti-oncogene; Repeat. | | |
| KW | SIGNAL 1 22 | | |
| FT | CHAIN 23 942 | | |
| FT | PROPEP 943 971 | | |
| FT | LIPID 942 942 | | |
| FT | DOMAIN 632 677 | | |
| FT | DOMAIN 708 750 | | |
| FT | DOMAIN 753 787 | | |
| FT | DOMAIN 37 338 | | |
| FT | 5 X KNOT REPEATS. | | |

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FT REPEAT 37 84 KNOT 1.
FT REPEAT 104 141 KNOT 2.
FT REPEAT 151 197 KNOT 3.
FT REPEAT 216 263 KNOT 4.
FT REPEAT 292 338 KNOT 5.
FT DISULFID 635 654 BY SIMILARITY.
FT DISULFID 633 658 BY SIMILARITY.
FT DISULFID 677 693 BY SIMILARITY.
FT CARBOHYD 39 39 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 971 AA, 106456 MW, 173D47D6AE6F834 CRC64;

Query Match 8.9%; Score 81; DB 1; Length 971;
Best Local Similarity 21.8%; Pred. No. 3.9;
Matches 32; Conservative 18; Mismatches 41; Indels 56; Gaps 8;

QY 34 CPEE-QYWDPL-----LQTC-----MSCKTICNHQSQRTCAFCRSIS 70
DB 74 CETWEIWNWCMNSLPGVFKKSDGMVGLGCCELATALECRQCKQASSKNDI----SKY 129
QY 71 CRKQCKFTDLRLDCIS-----CASTICGHPKCCATFCENKLRSPVNLPEELRQRS 123
DB 130 CRKE-----YENMLFSCISINEMGSCVCSYAGRH-TVCRVCQAIFFT----- 171
QY 124 GEVENSDNSGRYGLPEHRSSEAPAL 150
DB 172 ----DSSPSPQIKAVENYCAISIPOL 194

RESULT 11
TIE2_HUMAN STANDARD; PRT; 1124 AA.
AC 002763;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Angiopoietin 1 receptor precursor (BC 2.7.1.112) (Tyrosine-protein kinase receptor TIE-2) (Tyrosine-protein kinase receptor TEK) (1140 TEK) (hunica interna endothelial cell kinase) (CD202b antigen).
GN TEK OR TIE2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISUE=Placenta;
RX MEDLINE=93173509; PubMed=8382358;
RA Ziegler S.F., Bird T.A., Scherlinger J.A., Schooley K.A., Baum P.R.,
RT "Molecular cloning and characterization of a novel receptor protein tyrosine kinase from human placenta.",
RL Oncogene 8:663-670(1993).
RN [2]
RX MEDLINE=97134665; PubMed=8980225;
RA Vikkula M., Boon L.M., Carraway K.L. III, Calvert J.T., Diamond A.J.,
RA Goumnerov B., Paayk K.A., Marchuk D.A., Waman M.L., Cantley L.C.,
RA Mulliken J.B., Olse B.R.;
RT "Vascular dysmorphogenesis caused by an activating mutation in the receptor tyrosine kinase TIE2.",
RL Cell 87:1181-1190(1996).
RN [3]
RP VARIANTS VMC01 TRP-849 AND SER-897.
RX MEDLINE=9929243; PubMed=10369874;
RA Calvert J.T., Riney T.J., Kontos C.D., Cha E.H., Prieto V.G.,
RA Shee C.R., Berg J.N., Nevin N.C., Simpson S.A., Paayk K.A.,
RA Speer M.C., Peters K.G., Marchuk D.A.;
RT "Allelic and locus heterogeneity in inherited venous malformations,"
RT Hum. Mol. Genet. 8:1279-1289(1999).
CC -1- FUNCTION: THIS PROTEIN IS A PROTEIN TYROSINE-KINASE TRANSMEMBRANE

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CC RECEPTOR FOR ANGIOPOIETIN 1. IT MAY CONSTITUTE THE EARLIEST
CC MAMMALIAN ENDOTHELIAL CELL LINEAGE MARKER. PROBABLY REGULATES
CC ENDOTHELIAL CELL PROLIFERATION, DIFFERENTIATION AND GUIDES THE
CC PROPER PATTERNING OF ENDOTHELIAL CELLS DURING BLOOD VESSEL
CC FORMATION.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN ENDOTHELIAL CELLS
CC AND THEIR PROGENITORS, THE ANGIOBLASTS. HAS BEEN DIRECTLY FOUND
CC IN PLACENTA AND LUNG, WITH A LOWER LEVEL IN UMBILICAL VEIN
CC ENDOTHELIAL CELLS, BRAIN AND KIDNEY.
CC -1- DISEASE: DEFECTS IN TEK ARE A CAUSE OF DOMINANTLY INHERITED VENOUS
CC MALFORMATIONS (VMC01), AN ERROR OF VASCULAR MORPHOGENESIS
CC CHARACTERIZED BY DILATED, SERPIGINOUS CHANNELS.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. THE
CC SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- DATABASE: NAME=PROW, NOTE=PROW 3:12-14(2002);
CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/1715848914_g.htm".
CC
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CC
CC EMBL: L06139; AAA61139.1; -.
CC HSSP: P11362; IFGK.
CC Genew: HGNC:11724; TEK.
CC MIM: 600221; -.
CC MIM: 600195; -.
CC InterPro: IPR000561; EGF-like.
CC InterPro: IPR000719; Euk_Pkinase.
CC InterPro: IPR003961; FN_III.
CC InterPro: IPR001245; Tyr_Pkinase.
CC Pfam: PF00008; EGF_1.
CC Pfam: PF00041; fn3; 3.
CC Pfam: PF00069; Pkinase; 1.
CC PRINTS: PR00109; TYRKINASE.
CC ProDom: PD000001; Euk_Pkinase; 1.
CC SMART: SMO0181; EGF_2.
CC SMART: SMO0001; EGF_Like; 1.
CC SMART: SMO0060; FN3; 3.
CC SMART: SMO0219; Tyrc; 1.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
CC PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
CC PROSITE: PS00022; EGF_1; 3.
CC PROSITE: PS01186; EGF_2; 3.
CC Repeat: EGF-like domain; Transmembrane; Immunoglobulin domain;
CC Glycoprotein; Phosphorylation; Multigene family; Disease mutation.
CC SIGNAL 1 18
CC CHAIN 19 1124 ANGIOPOIETIN 1 RECEPTOR.
CC TRANSIN 19 745 EXTRACELLULAR (POTENTIAL).
CC TRANSSEM 746 770 POTENTIAL.
CC DOMAIN 771 1124 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 44 102 IG-LIKE C2-TYPE DOMAIN 1.
CC DOMAIN 210 252 EGF-LIKE 1.
CC DOMAIN 254 299 EGF-LIKE 2.
CC DOMAIN 301 341 EGF-LIKE 3.
CC DOMAIN 424 424 IG-LIKE C2-TYPE DOMAIN 2.
CC DOMAIN 444 536 FIBRONECTIN TYPE-III 1.
CC DOMAIN 541 634 FIBRONECTIN TYPE-III 2.
CC DOMAIN 638 732 FIBRONECTIN TYPE-III 3.
CC DOMAIN 824 1096 PROTEIN KINASE.
CC NP_BIND 830 838 ATP (BY SIMILARITY).
CC BINDING 855 855 ATP (BY SIMILARITY).

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FT ACT_SITE 964 964 BY SIMILARITY.
 FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 399 399 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 464 464 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 560 560 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 596 596 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 649 649 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 691 691 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MOD RES 992 992 PHOSPHORYLATION (AUTO-).
 FT VARIANT 849 849 R->W (IN VMCM1; ACTIVATING EFFECT).
 FT VARIANT 897 897 /FTID=VAR_006352.
 FT VARIANT 897 897 Y->S (IN VMCM1; ACTIVATING EFFECT).
 FT VARIANT 897 897 /FTID=VAR_008716.
 SQ SEQUENCE 1124 AA; 125810 MW; 65BC05D18FA4CCEC CRC64;
 Query Match 8.9%; Score 81; DB 1; Length 1124;
 Best Local Similarity 24.2%; Pred. No. 4.5;
 Matches 39; Conservative 15; Mismatches 63; Indels 44; Gaps 8;
 QY 26 WTGVAMRSCPEBYWDP---LIGTCM-----SCKTICN-HQSQ 59
 DB 203 FTRLVRC-EAQMGPBCNHLCTACMNNVCHEDTGECICPPGMGRTCEACELHTFG 261
 QY 60 RTCAFAFCRLSCREKGFYDHLRLDCISCAICGHPKQCAFPCENKLRSPVNLPELR 119
 DB 262 RTCKRCRGSG---DEGCKSYVFCFLDPYGCSCATGMKGLQCNEACH-----PGFYGPDK 312
 QY 120 RQSGEVENNSDNGRYGQLEHRSBPALFGLKLADQV 160
 DB 313 LRCSC---NNGEMCDRFQ-----GCLCSFGMGLQCEREGI 345
 RESULT 12
 ID PAC4 RAT STANDARD; PRT; 937 AA.
 AC Q63415;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Paired basic amino acid cleaving enzyme 4 precursor (EC 3.4.21.-)
 DE (Subtilisin/kexin-like protease PAC4) (Subtilisin-like proprotein
 DE convertase 4) (SPC4).
 GN PAC4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STAIN-Sprague-Dawley; Tissue-Hypothalamus, and Pituitary;
 RX MEDLINE=94349873; PubMed=8070361;
 RA Johnson R.C., Darlington D.N., Hand T.A., Bloomquist B.T., Mains R.E.,
 RT "PAC4: a subtilisin-like endoprotease prevalent in the anterior
 RT pituitary and regulated by thyroid status";
 RL Endocrinology 135:1178-1185 (1994).
 CC -1- FUNCTION: LIKELY TO REPRESENT AN ENDOPEPTASE ACTIVITY WITHIN THE
 CC CONSTITUTIVE SECRETORY PATHWAY, WITH UNIQUE RESTRICTED
 CC DISTRIBUTION IN BOTH NEUROENDOCRINE AND NON-NEUROENDOCRINE TISSUES
 CC AND CAPABLE OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF.
 CC -1- CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR
 CC PROPEPTIDE BY CLEAVAGE OF ARG-XAA-YAA-ARG-|-ZAA BONDS,
 CC WHERE XAA CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.
 CC -1- COFACTOR: PROBABLY CALCIUM-DEPENDENT (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: HIGH EXPRESSION IN THE ANTERIOR PITUITARY AND
 CC IN SEVERAL BRAIN REGIONS, THE ATRIUM, AND THE VENTRICLE.
 CC -1- DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE
 CC ASSISTING THE FOLDING OF THE ZMOGEN WITHIN THE ENDOPLASMIC
 CC RETICULUM.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.
 CC -1- SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.

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 CC -----
 DR EMBL; L31894; AAA61987.1; -.
 DR HSSP; Q99405; IMPT.
 DR MEROPS; S08_075; -.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR002174; Furin-like.
 DR InterPro; IPR002884; P domain.
 DR InterPro; IPR000209; Peptidase S8.
 DR Pfam; PF00082; Peptidase S8; 1.
 DR Pfam; PF01483; P-PARTIAL.
 DR PRINTS; PR00723; SUBTILISIN.
 DR ProDom; PD000717; P domain; 1.
 DR SMART; SM00181; EGF; 1.
 DR SMART; SM00261; FU; 5.
 DR PROSITE; PS00136; SUBTILASE ASP; 1.
 DR PROSITE; PS00137; SUBTILASE HIS; 1.
 DR PROSITE; PS00138; SUBTILASE SER; 1.
 KW Hydrolyase; Serine protease; Glycoprotein; Zymogen; Signal; Calcium;
 KW Cleavage on pair of basic residues; Repeat.
 FT SIGNAL 1 45
 FT PROPEP 46 132
 FT CHAIN 133 937
 FT DOMAIN 133 454
 FT DOMAIN 477 615
 FT DOMAIN 680 937
 FT SITE 132 133
 FT SITE 132 133
 FT SITE 534 536
 FT ACT_SITE 186 186
 FT ACT_SITE 227 227
 FT ACT_SITE 401 401
 FT CARBOHYD 240 240
 FT CARBOHYD 882 882
 FT CARBOHYD 900 900
 SQ SEQUENCE 937 AA; 104053 MW; F3865557C33705C8 CRC64;
 Query Match 8.9%; Score 80.5; DB 1; Length 937;
 Best Local Similarity 24.1%; Pred. No. 4.2;
 Matches 27; Conservative 17; Mismatches 45; Indels 23; Gaps 5;
 QY 16 DQERFPGGLTGVAMRSCPEBYWDPILIGTCMCK--TICNHOSQRTCAAFCSLSCKR 73
 DB 654 EEEERY-----TGVCHPFCGDKGCGPSADQCLNCHPSLGSKTRKVCSEB----- 701
 QY 74 BQKRYDHLRLDCISCAIC--GQHPKQ-----AFPCENKLRSPVNLPELR 116
 DB 702 PLGYGDTAARCRCHKGCETGTSRPTGLCSRGFGYHNOETWTVLLCP 753
 RESULT 13
 ID LMB3 HUMAN STANDARD; PRT; 1172 AA.
 AC Q13751; Q14733; Q14947; Q9UUK4; Q9UUL1;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Laminin beta-3 chain precursor (laminin 5 beta 3) (Laminin Bk chain)
 DE (Laminin B1 chain).
 GN LAMB3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95293372; PubMed=774918;

RA Pulkkinen L., Gerecke D.R., Christiano A.M., Wagman D.W.,
 RA Burgeson R.E., Uitto J.;
 RT "Cloning of the beta 3 chain gene (LAMB3) of human laminin 5, a
 RT candidate gene in junctional epidermolysis bullosa.";
 RL Genomics 25:192-198(1995).
 RN [2]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 172-190.
 RX MEDLINE=94209274; PubMed=7512558;
 RA Gerecke D.R., Wagman D.W., Champilaud M.F., Burgeson R.E.;
 RT "The complete primary structure for a novel laminin chain, the
 RT laminin Bk chain.";
 RL J. Biol. Chem. 269:11073-11080(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21221101; PubMed=11296269;
 RA Robbins P.B., Lin Q., Goodnough J.B., Tian H., Chen X., Khavari P.A.;
 RT "In vivo restoration of laminin 5 beta 3 expression and function in
 RT functional epidermolysis bullosa.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:5193-5198(2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Epidermis;
 RX MEDLINE=96015057; PubMed=8530036;
 RA Morishima Y., Arizawa T., Yamashita K., Abe T., Ueda E., Yasuno H.,
 RA Inazawa J.;
 RT "Chromosomal loci of 50 human keratinocyte cDNAs assigned by
 RT fluorescence in situ hybridization.";
 RL Genomics 28:273-279(1995).
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Graham D.;
 RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP VARIANT JEB LEU-679.
 RX MEDLINE=96055522; PubMed=7550237;
 RA Pulkkinen L., McGrath J.A., Christiano A.M., Uitto J.;
 RT "Detection of sequence variants in the gene encoding the beta 3 chain
 RT of laminin 5 (LAMB3).";
 RL Hum. Mutat. 6:77-84(1995).
 RN [7]
 RP VARIANT GABEB LYS-210.
 RX MEDLINE=99068967; PubMed=9767254;
 RA Mellerio J.E., Eady R.A., Atherton D.J., Lake B.D., McGrath J.A.;
 RT "E210K mutation in the gene encoding the beta3 chain of laminin-5
 RT (LAMB3) is predictive of a phenotype of generalized atrophic benign
 RT epidermolysis bullosa.";
 RL Br. J. Dermatol. 139:325-331(1998).
 CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
 CC is thought to mediate the attachment, migration, and organization
 CC of cells into tissues during embryonic development by interacting
 CC with other extracellular matrix components.
 CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
 CC different polypeptide chains (alpha, beta, gamma), which are bound
 CC to each other by disulfide bonds into a cross-shaped molecule
 CC comprising one long and three short arms with globules at each
 CC end.
 CC THE BETA-3 CHAIN IS A SUBUNIT OF LAMININ-5 (EPILGRIN/KALININ/
 CC NICEIN).
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR
 CC COMPONENT).
 CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
 CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
 CC -1- DOMAIN: DOMAIN VI IS GLOBULAR.
 CC -1- DISEASE: DEFECTS IN LAMB3 ARE A CAUSE OF JUNCTIONAL EPIDERMOLYSIS
 CC BULLOSA (JEB GRAVIS, ALSO KNOWN AS HERLITZ TYPE JEB. IT IS A
 CC BLISTERING DISORDER IN SKIN THAT IS CHARACTERIZED BY A SEPARATION
 CC OF BASAL CELLS FROM THE BASEMENT MEMBRANE DUE TO A DECREASED
 CC NUMBER OF HEMIDESMOSOMES. LAMININ-5 IS MISSING FROM THE BASEMENT
 CC MEMBRANE OF PATIENTS WITH THE GRAVIS FORM OF EPIDERMOLYSIS
 CC BULLOSA.
 CC -1- DISEASE: DEFECTS IN LAMB3 ARE A CAUSE OF GENERALIZED ATROPHIC
 CC BENIGN EPIDERMOLYSIS BULLOSA (GABEB). THIS NONLETHAL FORM OF

CC JUNCTIONAL EPIDERMOLYSIS BULLOSA IS CHARACTERIZED BY LIFE-LONG
 CC BLISTERING OF THE SKIN, ASSOCIATED WITH HAIR AND TOOTH
 CC ABNORMALITIES.
 CC -1- SIMILARITY: CONTAINS 6 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
 CC -1- SIMILARITY: CONTAINS 1 LAMININ EGF-LIKE DOMAINS.
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 CC -----
 CC EMBL; U17760; AAC51352.1; -;
 CC EMBL; U17745; AAC51352.1; JOINED.
 CC EMBL; U17746; AAC51352.1; JOINED.
 CC EMBL; U17747; AAC51352.1; JOINED.
 CC EMBL; U17748; AAC51352.1; JOINED.
 CC EMBL; U17749; AAC51352.1; JOINED.
 CC EMBL; U17750; AAC51352.1; JOINED.
 CC EMBL; U17751; AAC51352.1; JOINED.
 CC EMBL; U17752; AAC51352.1; JOINED.
 CC EMBL; U17753; AAC51352.1; JOINED.
 CC EMBL; U17754; AAC51352.1; JOINED.
 CC EMBL; U17755; AAC51352.1; JOINED.
 CC EMBL; U17756; AAC51352.1; JOINED.
 CC EMBL; U17757; AAC51352.1; JOINED.
 CC EMBL; U17758; AAC51352.1; JOINED.
 CC EMBL; U17759; AAC51352.1; JOINED.
 CC EMBL; L25541; AA61834.1; -;
 CC EMBL; AY035763; AA61364.1; -;
 CC EMBL; D37766; BAA22263.1; -;
 CC EMBL; AL031316; CAB40149.1; -;
 CC EMBL; AL023754; CAA19297.1; -;
 CC HSSP; P02468; 1KIO.
 CC GeneW; HGNC:6490; LAMB3.
 CC MIM; 150310; -;
 CC MIM; 22650; -;
 CC MIM; 226700; -;
 CC InterPro; IPR000561; EGF-like.
 CC InterPro; IPR001886; LAMNT.
 CC InterPro; IPR002049; Laminin EGF.
 CC Pfam; PF00053; laminin EGF 6.
 CC Pfam; PF00055; laminin Nterm. 1.
 CC PRINTS; PR00011; EGF/LAMININ.
 CC ProDom; PD002082; LAMNT. 1.
 CC SMART; SM00180; EGF_Lam. 6.
 CC SMART; SM00136; LAMNT. 1.
 CC PROSITE; PS00022; EGF_1; 5.
 CC PROSITE; PS01186; EGF_2; 1.
 CC PROSITE; PS01248; LAMININ TYPE EGF; 5.
 CC GlycoProfile; Basement membrane; Extracellular matrix; Coiled coil;
 CC Laminin EGF-like domain; Cell adhesion; Repeat; Signal;
 CC Disease mutation; Epidermolysis bullosa.
 CC SIGNAL 1 17
 CC FT CHAIN 18 249 LAMININ BETA-3 CHAIN.
 CC FT DOMAIN 18 249 LAMININ N-TERMINAL (DOMAIN VI).
 CC FT DOMAIN 250 315 LAMININ EGF-LIKE 1.
 CC FT DOMAIN 316 378 LAMININ EGF-LIKE 2.
 CC FT DOMAIN 379 430 LAMININ EGF-LIKE 3.
 CC FT DOMAIN 431 480 LAMININ EGF-LIKE 4.
 CC FT DOMAIN 481 533 LAMININ EGF-LIKE 5.
 CC FT DOMAIN 534 578 LAMININ EGF-LIKE 6.
 CC FT DOMAIN 579 785 DOMAIN II.
 CC FT DOMAIN 786 816 DOMAIN ALPHA.
 CC FT DOMAIN 817 1170 DOMAIN I.
 CC FT DOMAIN 723 1170 COILED COIL (POTENTIAL).
 CC FT DOMAIN 831 884 COILED COIL (POTENTIAL).
 CC FT DOMAIN 948 1133 COILED COIL (POTENTIAL).
 CC FT DISULFD 250 259 BY SIMILARITY.
 CC FT DISULFD 252 279 BY SIMILARITY.
 CC FT DISULFD 281 290 BY SIMILARITY.

| Query Match | Best Local Similarity | Score | DB | Length |
|---|-----------------------|-------|--------|----------|
| Matches 41; Conservative | 25.3%; | 79.5; | 1; | 1172; |
| | 16; Mismatches | 66; | Indels | 39; Gaps |
| 19 ERPPGLMTGVAMRSCPEQYWDPLLTGTGMSCKTICNHQSQRCAFCRSLSC-RKEGG 76 | 19 | 124 | 124 | 124 |
| 504 EEPFGIMCSAAAIRKCPDRTTGDVATG-----CRACDDEFGTGG 543 | 504 | 269 | 269 | 269 |
| 77 KEVDHLRDCISASCIGQHPRKQCAV-FCENKLRSPV-----NLPEELRQ-RSG 124 | 77 | 388 | 388 | 388 |
| 544 PCGDKASGRCLORPGLTGRCDQCQNGYCN---RYVVCVAACHPCPOTYADLRBQALRFG 600 | 544 | 427 | 427 | 427 |
| 125 EYVENSNDNSGRYQGLHRSSEASPALPGLKLSADQVALYST 166 | 125 | 441 | 441 | 441 |
| 601 RLNRNATASLMSGPELEDRGL-ASRLIDA-KSKIEQIRAVLSS 640 | 601 | 500 | 500 | 500 |
| | | 603 | 603 | 603 |
| | | 815 | 815 | 815 |
| Query Match | Best Local Similarity | Score | DB | Length |
| Matches 41; Conservative | 25.3%; | 79.5; | 1; | 1172; |
| | 16; Mismatches | 66; | Indels | 39; Gaps |
| 19 ERPPGLMTGVAMRSCPEQYWDPLLTGTGMSCKTICNHQSQRCAFCRSLSC-RKEGG 76 | 19 | 124 | 124 | 124 |
| 504 EEPFGIMCSAAAIRKCPDRTTGDVATG-----CRACDDEFGTGG 543 | 504 | 269 | 269 | 269 |
| 77 KEVDHLRDCISASCIGQHPRKQCAV-FCENKLRSPV-----NLPEELRQ-RSG 124 | 77 | 388 | 388 | 388 |
| 544 PCGDKASGRCLORPGLTGRCDQCQNGYCN---RYVVCVAACHPCPOTYADLRBQALRFG 600 | 544 | 427 | 427 | 427 |
| 125 EYVENSNDNSGRYQGLHRSSEASPALPGLKLSADQVALYST 166 | 125 | 441 | 441 | 441 |
| 601 RLNRNATASLMSGPELEDRGL-ASRLIDA-KSKIEQIRAVLSS 640 | 601 | 500 | 500 | 500 |
| | | 603 | 603 | 603 |
| | | 815 | 815 | 815 |
| Query Match | Best Local Similarity | Score | DB | Length |
| Matches 41; Conservative | 25.3%; | 79.5; | 1; | 1172; |
| | 16; Mismatches | 66; | Indels | 39; Gaps |
| 19 ERPPGLMTGVAMRSCPEQYWDPLLTGTGMSCKTICNHQSQRCAFCRSLSC-RKEGG 76 | 19 | 124 | 124 | 124 |
| 504 EEPFGIMCSAAAIRKCPDRTTGDVATG-----CRACDDEFGTGG 543 | 504 | 269 | 269 | 269 |
| 77 KEVDHLRDCISASCIGQHPRKQCAV-FCENKLRSPV-----NLPEELRQ-RSG 124 | 77 | 388 | 388 | 388 |
| 544 PCGDKASGRCLORPGLTGRCDQCQNGYCN---RYVVCVAACHPCPOTYADLRBQALRFG 600 | 544 | 427 | 427 | 427 |
| 125 EYVENSNDNSGRYQGLHRSSEASPALPGLKLSADQVALYST 166 | 125 | 441 | 441 | 441 |
| 601 RLNRNATASLMSGPELEDRGL-ASRLIDA-KSKIEQIRAVLSS 640 | 601 | 500 | 500 | 500 |
| | | 603 | 603 | 603 |
| | | 815 | 815 | 815 |

| | |
|----|--|
| Rc | TISSUE=Ovary; |
| RX | MEDLINE=95183490; PubMed=7878005; |
| RA | Schonbaum C.P., Lee S., Mahowald A.P.; |
| RT | "The Drosophila yolkless gene encodes a vitellogenin receptor belonging to the low density lipoprotein receptor superfamily."; |
| RL | Proc. Natl. Acad. Sci. U.S.A. 92:1485-1489(1995). |
| CC | -1- FUNCTION: INVOLVED IN UPTAKE OF VITELLOGENIN BY ENDOCYTOSIS. |
| CC | -1- SIMILARITY: CONTAINS 13 LDL-RECEPTOR CLASS A DOMAINS. |
| CC | -1- SIMILARITY: CONTAINS 7 EGF-LIKE DOMAINS. |
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| CC | ----- |
| DR | EMBL; U13637; AAB60217.1; -. |
| DR | HSSP; P01130; IAUJ. |
| DR | PfBase: PF0004649; YL. |
| DR | InterPro; IPRO00152; Asx_hydroxyl. |
| DR | InterPro; IPRO00561; EGF-like. |
| DR | InterPro; IPRO02172; LDL_recept_A. |
| DR | InterPro; IPRO00033; ldl_receptor_rep. |
| DR | pfam; PF00008; EGF_5. |
| DR | pfam; PF00057; ldl_recept_a; 13. |
| DR | pfam; PF00058; ldl_recept_b; 6. |
| DR | PRINTS; PR00261; LDLRECEPTOR. |
| DR | SMART; SM00179; EGF_CA; 2. |
| DR | SMART; SM00001; EGF_like; 4. |
| DR | SMART; SM00192; LDLA_13. |
| DR | SMART; SM00135; LY; 8. |
| DR | PROSITE; PS00010; ASX_HYDROXYL; 2. |
| DR | PROSITE; PS01186; EGF_2; 3. |
| DR | PROSITE; PS01187; EGF_CA; 2. |
| DR | PROSITE; PS01209; LDLFA_1; 11. |
| DR | PROSITE; PSS0068; LDLRA_2; 13. |
| KW | Glycoprotein; Signal; Transmembrane; EGF-like domain; Receptor; |
| KM | Repeat; Endocytosis. |
| FT | SIGNAL 1 ? |
| FT | CHAIN ? 1984 |
| FT | DOMAIN ? 1800 |
| FT | TRANSMEM 1801 1821 |
| FT | DOMAIN 1822 1984 |
| FT | DOMAIN 88 126 |
| FT | DOMAIN 127 167 |
| FT | DOMAIN 182 222 |
| FT | DOMAIN 225 264 |
| FT | DOMAIN 264 306 |
| FT | DOMAIN 306 347 |
| FT | DOMAIN 348 388 |
| FT | DOMAIN 660 701 |
| FT | DOMAIN 984 1026 |
| FT | DOMAIN 1029 1064 |
| FT | DOMAIN 1072 1111 |
| FT | DOMAIN 1116 1154 |
| FT | DOMAIN 1156 1195 |
| FT | DOMAIN 1196 1234 |
| FT | DOMAIN 1241 1281 |
| FT | DOMAIN 1281 1320 |
| FT | DOMAIN 1338 1377 |
| FT | DOMAIN 1375 1417 |
| FT | DOMAIN 1418 1457 |
| FT | DOMAIN 1734 1770 |
| FT | SITE 1837 1837 |
| FT | SITE 1878 1878 |
| FT | SITE 1892 1892 |
| FT | DISULFID 90 102 |
| FT | DISULFID 97 115 |
| FT | DISULFID 109 124 |
| FT | BY SIMILARITY. |
| FT | BY SIMILARITY. |
| FT | BY SIMILARITY. |
| FT | CYTOPLASMIC (POTENTIAL). |
| FT | LIDL-RECEPTOR CLASS A 1. |
| FT | LIDL-RECEPTOR CLASS A 2. |
| FT | LIDL-RECEPTOR CLASS A 3. |
| FT | LIDL-RECEPTOR CLASS A 4. |
| FT | LIDL-RECEPTOR CLASS A 5. |
| FT | EGF-Like 1. |
| FT | EGF-Like 2. |
| FT | EGF-Like 3. |
| FT | EGF-Like 4. |
| FT | LIDL-RECEPTOR CLASS A 6. |
| FT | LIDL-RECEPTOR CLASS A 7. |
| FT | LIDL-RECEPTOR CLASS A 8. |
| FT | LIDL-RECEPTOR CLASS A 9. |
| FT | LIDL-RECEPTOR CLASS A 10. |
| FT | LIDL-RECEPTOR CLASS A 11. |
| FT | LIDL-RECEPTOR CLASS A 12. |
| FT | LIDL-RECEPTOR CLASS A 13. |
| FT | EGF-Like 5. |
| FT | EGF-Like 6. |
| FT | EGF-Like 7. |
| FT | CRITICAL FOR ENDOCYTOSIS (POTENTIAL). |
| FT | CRITICAL FOR ENDOCYTOSIS (POTENTIAL). |
| FT | CRITICAL FOR ENDOCYTOSIS (POTENTIAL). |
| FT | BY SIMILARITY. |
| FT | BY SIMILARITY. |
| FT | BY SIMILARITY. |


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FT DISULFID 129 144 BY SIMILARITY.
FT DISULFID 137 157 BY SIMILARITY.
FT DISULFID 151 166 BY SIMILARITY.
FT DISULFID 184 197 BY SIMILARITY.
FT DISULFID 191 210 BY SIMILARITY.
FT DISULFID 204 220 BY SIMILARITY.
FT DISULFID 227 239 BY SIMILARITY.
FT DISULFID 234 253 BY SIMILARITY.
FT DISULFID 247 262 BY SIMILARITY.
FT DISULFID 266 281 BY SIMILARITY.
FT DISULFID 275 294 BY SIMILARITY.
FT DISULFID 288 304 BY SIMILARITY.
FT DISULFID 310 321 BY SIMILARITY.
FT DISULFID 315 331 BY SIMILARITY.
FT DISULFID 333 346 BY SIMILARITY.
FT DISULFID 352 363 BY SIMILARITY.
FT DISULFID 359 372 BY SIMILARITY.
FT DISULFID 374 387 BY SIMILARITY.
FT DISULFID 664 673 BY SIMILARITY.
FT DISULFID 669 685 BY SIMILARITY.
FT DISULFID 687 700 BY SIMILARITY.
FT DISULFID 988 999 BY SIMILARITY.
FT DISULFID 995 1009 BY SIMILARITY.
FT DISULFID 1011 1025 BY SIMILARITY.
FT DISULFID 1031 1040 BY SIMILARITY.
FT DISULFID 1035 1053 BY SIMILARITY.
FT DISULFID 1047 1062 BY SIMILARITY.
FT DISULFID 1074 1087 BY SIMILARITY.
FT DISULFID 1081 1100 BY SIMILARITY.
FT DISULFID 1094 1109 BY SIMILARITY.
FT DISULFID 1118 1130 BY SIMILARITY.
FT DISULFID 1125 1143 BY SIMILARITY.
FT DISULFID 1137 1152 BY SIMILARITY.
FT DISULFID 1158 1170 BY SIMILARITY.
FT DISULFID 1165 1183 BY SIMILARITY.
FT DISULFID 1177 1193 BY SIMILARITY.
FT DISULFID 1198 1210 BY SIMILARITY.
FT DISULFID 1205 1223 BY SIMILARITY.
FT DISULFID 1217 1232 BY SIMILARITY.
FT DISULFID 1243 1257 BY SIMILARITY.
FT DISULFID 1250 1270 BY SIMILARITY.
FT DISULFID 1264 1279 BY SIMILARITY.
FT DISULFID 1283 1296 BY SIMILARITY.
FT DISULFID 1290 1309 BY SIMILARITY.
FT DISULFID 1303 1318 BY SIMILARITY.
FT DISULFID 1330 1352 BY SIMILARITY.
FT DISULFID 1347 1365 BY SIMILARITY.
FT DISULFID 1359 1375 BY SIMILARITY.
FT DISULFID 1379 1392 BY SIMILARITY.
FT DISULFID 1388 1401 BY SIMILARITY.
FT DISULFID 1403 1416 BY SIMILARITY.
FT DISULFID 1422 1432 BY SIMILARITY.
FT DISULFID 1438 1441 BY SIMILARITY.
FT DISULFID 1443 1456 BY SIMILARITY.
FT DISULFID 1738 1747 BY SIMILARITY.
FT DISULFID 1743 1756 BY SIMILARITY.
FT DISULFID 1758 1769 BY SIMILARITY.
FT CARBOHYD 30 30 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 35 35 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 429 429 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 666 666 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 749 749 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 782 782 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1022 1022 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1240 1240 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1265 1265 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1326 1326 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1475 1475 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1490 1490 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 1519 1519 V -> I.
SQ SEQUENCE 1984 AA; 219318 MW; F92A256B0ACD5E48 CRC64;

```

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Query Match 8.7%; Score 79.5; DB 1; Length 1984;
Best Local Similarity 29.9%; Pred. No. 11;
Matches 32; Conservative 7; Mismatches 41; Indels 27; Gaps 8;

Qy 26 WTGVAMRSCPEQWVDPLGTCMSCKTCN-----HQSRTCAACRSLS----- 70
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1333 WS-TSSRSC-RPHLPDCCDGECDVLSRVCCNFPDCTNGHDEGPKATYCRSASGRVCOH 1390
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 71 -CRKEQG---KFYD--HLNRDCISGASI--CGQHPKOCAYFCENKL 108
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1391 KCRATPAGAVCSCFPGYRLDADQKSCLDIDEC-QEQPCAOUCENTL 1436
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
ID 2147 HUMAN STANDARD; PRT; 630 AA.
AC 014258;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Zinc finger protein 147 (Estrogen responsive finger protein) (Efp).
GN ZNF147 OR EFP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=94068555; PubMed=8248217;
RA Inoue S., Oriimo A., Hosoi T., Kondo S., Toyoshima H., Kondo T.,
RA Ikegami A., Ouchi Y., Oriimo H., Muramatsu M.;
RT "Genomic binding-site cloning reveals an estrogen-responsive gene that
RT encodes a Ring finger protein."
RN Proc. Natl. Acad. Sci. U.S.A. 90:11117-11121(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC - FUNCTION: MEDIATES ESTROGEN ACTION IN VARIOUS TARGET ORGANS.
CC - TISSUE SPECIFICITY: UBICUITOUS.
CC - SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC - SIMILARITY: CONTAINS 1 SPRY DOMAIN.
-----
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DR EMBL; D21205; BA004747.1; -.
DR EMBL; BC016924; AAH16924.1; -.
DR GenBank; HGNC:12932; ZNF147.
DR MIM; 600453; -.
DR InterPro; IPR001870; Gamma_carboxylase.
DR InterPro; IPR003878; SPRY_domain.
DR InterPro; IPR003877; SPRY_receptor.
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00097; ZF-C3HC4; 1.
DR Pfam; PF00622; SPRY; 1.
DR SMART; SM00184; RING; 1.
DR SMART; SM00449; SPRY; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Zinc-finger; Coiled coil.
FT ZN FING 13 54 RING-TYPE.
FT DOMAIN 217 307 COILED COIL (POTENTIAL).
FT DOMAIN 509 630 SPRY.
SQ SEQUENCE 630 AA; 70989 MW; BE4EE713F96DD080 CRC64;

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Query Match 8.6%; Score 78.5; DB 1; Length 630;
Best Local Similarity 23.0%; Pred. No. 4.4;
Matches 38; Conservative 20; Mismatches 54; Indels 53; Gaps 9;

QY 22 PQGLMTGVAMSGPBEQYWDPIILGTOMSGKTIQNH-----QSQRTC-----AARCRS-LSGR 72
Db 86 PADVTPPPARASAPSP-----NAQVACDHCLKKAAVKTCLVCMASFQCEHLOPH 134
QY 73 KEQGFYDHL-----RDCISCASICGHPKQCAVFC-----ENKLRSPVNL 115
Db 135 FDSPPAFQDHPLOHPVRDL--RRKCSQHNRLREFFCPHSEICICLVEHKTCSPASL- 191
QY 116 PELRRQSGEVENNSDNGRYQGLEHRSSEASPALPGLKLSADQV 160
Db 192 ----SQASADLEAT-----LRHKLTVMYSQINGASRALDV 223

Search completed: February 4, 2003, 12:58:12
Job time : 14.4251 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using SW model

Run on: February 4, 2003, 12:56:21 / Search time 19.4899 Seconds
(without alignments)
818.800 Million cell updates/sec

Title: US-09-854-864-15

Perfect score: 909

Sequence: 1 MSGIGRSGRRGGRSRVDOEER.....SPALPGKLSADQVALVYST 166

Scoring table: BIOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR_73:*

1: pirl:*

2: pirl2:*

3: pirl3:*

4: pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|---------------------|
| 1 | 97.5 | 10.7 | 1548 | 2 S34583 | serine proteinase |
| 2 | 86.5 | 9.5 | 353 | 2 T06466 | cathepsin B-like C |
| 3 | 86 | 9.5 | 1299 | 2 T43251 | furin (EC 3.4.21.7 |
| 4 | 84.5 | 9.3 | 355 | 2 AD0299 | conserved hypothet |
| 5 | 83 | 9.1 | 13288 | 2 T03099 | muscin, submaxillar |
| 6 | 82.5 | 9.1 | 899 | 2 G02428 | subtilisin-like pr |
| 7 | 82.5 | 9.1 | 915 | 2 JC6148 | subtilisin-like pr |
| 8 | 82 | 9.0 | 932 | 2 T52527 | PACE4A - mouse (fr |
| 9 | 82 | 9.0 | 1650 | 2 S53457 | dominant autoantig |
| 10 | 82 | 9.0 | 4660 | 2 T42737 | gp330 protein prec |
| 11 | 81 | 8.9 | 773 | 1 JH0609 | protein-tyrosine-p |
| 12 | 81 | 8.9 | 1124 | 1 I58388 | gene PAC64 protein |
| 13 | 80.5 | 8.9 | 937 | 2 I53282 | hypothetical prote |
| 14 | 80 | 8.8 | 108 | 2 H69834 | hypothetical prote |
| 15 | 80 | 8.8 | 330 | 2 T25169 | hypothetical prote |
| 16 | 80 | 8.8 | 996 | 2 JB0237 | apolipoprotein B r |
| 17 | 79.5 | 8.7 | 1984 | 2 T13171 | probable vitelloge |
| 18 | 79 | 8.7 | 269 | 2 C69312 | molybdopterin oxid |
| 19 | 78.5 | 8.6 | 630 | 2 A49656 | estrogen-responsiv |
| 20 | 78.5 | 8.6 | 1170 | 2 A53612 | laminin B1 chain |
| 21 | 78 | 8.6 | 596 | 2 A45664 | variant-specific s |
| 22 | 77.5 | 8.5 | 230 | 2 T19364 | hypothetical prote |
| 23 | 77.5 | 8.5 | 2195 | 2 T34264 | hypothetical prote |
| 24 | 77.5 | 8.5 | 2871 | 2 A55624 | fibrillin-1 precur |
| 25 | 77 | 8.5 | 620 | 2 AF0273 | probable iron-sulf |
| 26 | 77 | 8.5 | 751 | 2 T15230 | hypothetical prote |
| 27 | 77 | 8.5 | 1184 | 2 T09484 | cartilage intermed |
| 28 | 76.5 | 8.4 | 1680 | 2 A43434 | furin (EC 3.4.21.7 |
| 29 | 76.5 | 8.4 | 1872 | 2 JC4976 | plexin 3 precursor |

| | | | | | |
|----|------|-----|------|----------|--------------------|
| 30 | 76 | 8.4 | 367 | 2 T45812 | dnaU-like protein |
| 31 | 76 | 8.4 | 574 | 2 B88465 | protein B024.8 (i |
| 32 | 76 | 8.4 | 915 | 2 B48225 | probable proprotei |
| 33 | 76 | 8.4 | 1748 | 2 S42136 | cnjB protein - Tet |
| 34 | 75.5 | 8.3 | 427 | 2 S38032 | hypothetical prote |
| 35 | 75.5 | 8.3 | 1620 | 2 T27283 | hypothetical prote |
| 36 | 75 | 8.3 | 962 | 2 JC5571 | subtilisin-like pr |
| 37 | 75 | 8.3 | 969 | 1 A39490 | subtilisin-like pr |
| 38 | 75 | 8.3 | 975 | 2 JC5570 | subtilisin-like pr |
| 39 | 75 | 8.3 | 2664 | 2 T28626 | variant-specific s |
| 40 | 75 | 8.3 | 3002 | 2 A47221 | fibrillin 1 precur |
| 41 | 75 | 8.3 | 4544 | 1 S02392 | alpha-2-macroglobu |
| 42 | 75 | 8.3 | 4545 | 1 S25111 | alpha-2-macroglobu |
| 43 | 74.5 | 8.2 | 382 | 1 S48748 | protein-tyrosine-p |
| 44 | 74.5 | 8.2 | 501 | 2 T61512 | TNF receptor assoc |
| 45 | 74.5 | 8.2 | 773 | 2 I46059 | beta-1 integrin su |

ALIGNMENTS

RESULT 1

S34583 serine proteinase (EC 3.4.21.-) PC6B - mouse

C/Species: Mus musculus (house mouse)

C/Date: 02-Dec-1993 #sequence #revision 10-Nov-1995 #text_change 05-Nov-1999

C/Accession: S34583

R:Nakagawa, T.; Murakami, K.; Nakayama, K.

FEBS Lett. 327, 165-171, 1993

A/Title: Identification of an isoform with an extremely large Cys-rich region of PC6, a

A/Reference number: S34583; MUID:9327934; PMID:8335106

A/Accession: S34583

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1548 <NA>

A/References: GB:DI7563; NID:g407344; PIDN:BAA04507.1; PID:d1005033; PID:g440374

C/Keywords: hydrolase; serine proteinase

Query Match 10.7%; Score 97.5; DB 2; Length 1548;

Best Local Similarity 30.2%; Pred. No. 1; Matches 29; Conservative 12; Mismatches 32; Indels 23; Gaps 7;

QY 14 RVDQ--EERFPGIMTVGAMRSCEEQYWDPLG--TCMSCKTICN-----HQSGRTCAAF 65

DB 627 RADKHGGRF---LYHGSCLENCVPGHY--PAKHGTCLPCDNCBELCVNPHICSRCMGSGY 681

QY 66 -----CRSLSCRKKEQKFTYDHLRDCTISCASIC 93

DB 682 VIIPNHTCKLCKR--QGEFQDSEYECWCEEGC 715

RESULT 2

T06466 cathepsin B-like cysteine proteinase (EC 3.4.22.-) (clone A116) - wheat (fragment)

C/Species: Triticum aestivum (common wheat)

C/Date: 23-Apr-1999 #sequence #revision 23-Apr-1999 #text_change 11-May-2000

C/Accession: T06466

R:Cejudo, F.J.; Murphy, G.; Chirnov, C.; Baulcombe, D.C.

Plant J. 2, 937-948, 1992

A/Title: A gibberellin-regulated gene from wheat with sequence homology to cathepsin B c

A/Reference number: Z15659; MUID:93258430; PMID:1302642

A/Accession: T06466

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-953 <CE>

A/Cross-references: EMBL:X66013; NID:g21698; PIDN:CAA46811.1; PID:g21699

A/Experimental source: cv. Chinese Spring, etiolated shoots

C/Genetics:

A/Note: Intron positions not resolved (incomplete sequence)

C/Superfamily: papain

C/Keywords: cysteine proteinase; glycoprotein; hydrolase

Query Match 9.5%; Score 86.5; DB 2; Length 353;

Best Local Similarity 24.7%, Pred. No. 2.7,
Matches 36; Conservative 12; Mismatches 63; Indels 35; Gaps 5;

Qy 22 PGLMTGVMARSCEP-----EQYWDPLGTCMSCKTTCNHOSORTCAAFCRSLSCR 72
Db 80 PGLMTGVMARSCEP-----EQYWDPLGTCMSCKTTCNHOSORTCAAFCRSLSCR 132
Qy 73 KEQKRYVDHL-----LRDCISCAISCGHPKQCAVFCENKLRSPVNLPELRRORSGE 125
Db 133 ALQDRFCILHMSVSLVNDLAC-----CGFLCGSGNGGVPISAMRYFRSGV 182
Qy 126 VENNDSNGRYOGLERHRSASPALP 151
Db 183 VTBECDPYDQTCQHPGCE--PAYP 206

RESULT 3

T43251
Furin (EC 3.4.21.75) - fall armyworm

N/Alternate names: paired basic amino acid cleaving enzyme; proprotein convertase; serin
C/Species: Spodoptera frugiperda (fall armyworm)
C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000

C/Accession: T43251
R/Cleptik, M.; Klenk, H.
Submitted to the EMBL Data Library, January 1996

A/Description: Cloning and functional characterization of FURIN from Spodoptera frugiper
A/Reference number: 222368
A/Accession: T43251

A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA

A/Residues: 1-1299 <CIE>
A/Cross-references: EMBL:268888; NID:g1167859; PID:e219690; PID:CAA93116.1

A/Experimental source: clone sfurin 6; ovary
C/Function:

A/Description: responsible for the endoproteolytic processing of proproteins with specif
C/Keywords: hydrolase; serine proteinase

Query Match 9.5%; Score 86; DB 2; Length 1299;
Best Local Similarity 25.0%; Pred. No. 9.2;
Matches 39; Conservative 16; Mismatches 51; Indels 50; Gaps 9;

Qy 22 PGLMTGVMARSCEPQYWDPLGTCMSCKTTCNHOSORTCAAFCRSLSCRKEQKRF--- 78
Db 1104 PGLMTGVMARSCEPQYWDPLGTCMSCKTTCNHOSORTCAAFCRSLSCRKEQKRF--- 1148
Qy 79 -----YHLLRDCISCAISCG-----QHPKQCAVFCENKLRSPVNLPELRRORSGEYE 127
Db 1149 TCSRPLRIRLNNQCVPCSEKGVMTSTPTDCH--CN-----PE-----NGECL 1192
Qy 128 NNSDSNGRYOGLERHRSASPALPGLKLSADQVALV 163
Db 1193 NNS-VAGKRRIAEWGLAHTAPASD-----AAPSAVAV 1223

RESULT 4

AD0299
conserved hypothetical protein YPO2451 [imported] - Yersinia pestis (strain CO92)

C/Species: Yersinia pestis
C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 03-Nov-2001

C/Accession: AD0299
R/Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tiltball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Croft, A.; Davies, R.M.; Davis, P.; Dougan, G.;

11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
Nature 413, 523-527, 2001

A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A/Reference number: AB0001; MUID:21470413; PMID:11586360

A/Accession: AD0299
A/Status: preliminary

A/Molecule type: DNA
A/Residues: 1-355 <KUR>

A/Cross-references: GB:AL550842; PIDN:CA931256.1; PID:g15980445; GSPDB:GN00175
C/Genetic:

A/Gene: YPO2451

C/Superfamily: Escherichia coli yceA protein

Query Match 9.3%; Score 84.5; DB 2; Length 355;
Best Local Similarity 24.4%; Pred. No. 4;
Matches 30; Conservative 20; Mismatches 48; Indels 25; Gaps 5;

Qy 37 EQYWDPLGTCMSCKTTCNHOSORTCAAFCRSLSCRKEQKRYVDHLRDCISCAISCGH 96
Db 257 ERISDVIAHCHQCTPCDAHTN-----CKNDGC-----HL--FIQCPVCAAKF 299
Qy 97 PQKCAVFCENKLRSPVNLPELRRORSGEVENNSDSNGRYOGLERHRSASPALPGLKLS 156
Db 300 EECGSGQICQEBLK---LPEBQRSPRAGRENGIKIFNKSGL---LQATWHIPSPKS 351
Qy 157 ADQ 159
Db 352 ADB 354

RESULT 5

T03099
mucin, submaxillary - pig

N/Alternate names: apomucin
C/Species: Sus scrofa domestica (domestic pig)

C/Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 02-Jun-2000
C/Accession: T03099; A40009; A28528; B29789

R/Eckhardt, A.E.; Timpte, C.S.; Deluca, A.W.; Hill, R.L.
J. Biol. Chem. 272, 33204-33210, 1997

A/Title: The complete cDNA sequence and structural polymorphism of the polypeptide chain
A/Reference number: 214839; MUID:98070526; PMID:9407109

A/Accession: T03099
A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1328 <ECK>
A/Cross-references: EMBL:AF005273; NID:g2581863; PIDN:AA62527.1; PID:g2581864

R/Eckhardt, A.E.; Timpte, C.S.; Abernethy, J.L.; Zhao, Y.; Hill, R.L.
J. Biol. Chem. 266, 9678-9686, 1991

A/Title: Porcine submaxillary mucin contains a cysteine-rich, carboxyl-terminal domain in
A/Reference number: A40009; MUID:91236743; PMID:2033060

A/Accession: A40009
A/Molecule type: mRNA

A/Residues: 12139-12167, 'T', 12169-13288 <EC3>
A/Cross-references: GB:M21174; GB:03512; NID:g164321; PIDN:AAA30998.1; PID:g164374

R/Timpte, C.S.; Eckhardt, A.E.; Abernethy, J.L.; Hill, R.L.
J. Biol. Chem. 263, 1081-1088, 1988

A/Title: Porcine submaxillary gland apomucin contains tandemly repeated, identical seque
A/Reference number: A28528; MUID:88087170; PMID:2826455

A/Accession: A28528
A/Molecule type: mRNA

A/Residues: 12139-12167, 'T', 12169-12641 <TIM>
A/Cross-references: GB:M21174; GB:03512; NID:g164321; PIDN:AAA30990.1; PID:g552360

A/Experimental source: submaxillary gland
R/Eckhardt, A.E.; Timpte, C.S.; Abernethy, J.L.; Toumadje, A.; Johnson Jr., W.C.; Hill,

J. Biol. Chem. 262, 11339-11344, 1987
A/Title: Structural properties of porcine submaxillary gland apomucin.

A/Reference number: A92606; MUID:87280230; PMID:3611111
A/Accession: B29789

A/Molecule type: protein
A/Residues: 1572-1607 <EC2>
C/Superfamily: pig submaxillary mucin

C/Keywords: tandem repeat

Query Match 9.1%; Score 83; DB 2; Length 13288;
Best Local Similarity 23.5%; Pred. No. 1.3e+02;
Matches 32; Conservative 18; Mismatches 44; Indels 42; Gaps 8;

Qy 18 EERFQGLMTGVAMR-SCPEQYWD-----PLAETCMSCKTTCNHOSORTCAAFCRSL 70
Db 13075 EKKSPGDVWTANCHCTGTAKTVDCKRKEGSPPTCTGELRLIFKXANDTC---CEIGH 13131
Qy 71 CRK-----EGKRYVDHLRDCI--SCASL-----CGH-----PKQ 99
Db 13132 CEKRTCLFNNTDYEVGSSFPDPPNPNPCVTYSCONTGFTAVVONCPKQTCABEDRVYDSKO 13191

QY 100 CAYFENKLR-SPYNL 114
Db 13192 CCYTCKSSCKSPNNV 13207

RESULT 6

G02428
subtilisin-like proteolysin convertase (EC 3.4.21.-) 5 precursor - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Mar-2000
C/Accession: G02428
R:Reindelhuber, T.L.
submitted to the EMBL Data Library, February 1996
A/Reference number: H01442
A/Accession: G02428
A/Molecule type: mRNA
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Residues: 1-899 <REU>
A/Cross-references: EMBL:U09114; NID:g1218057; PIDN:AAA91807.1; PID:g1218058
C/Genetics:
A/Status: PCS
C/Superfamily: subtilisin-like protease PACE4; subtilisin homology
C/Keywords: hydrolase, serine proteinase
F:148-386/Domain: subtilisin homology <SBT>

Query Match 9.1%; Score 82.5; DB 2; Length 899;
Best Local Similarity 26.0%; Pred. No. 14;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;

QY 27 TGVAMRSCPEBQYWDPLIGTCMCKTICNHOSQRTCAAF-----CR-----SLSC 71
Db 703 TNSCVTHCPDGSYQDTKKNLCRKSENC-----KTCTEFHNCTECRDGLSLQSRCSVSC 757

QY 72 RKEGKPYDHLRDCISCSAIC-----GQHPKQC-----AYCEN 106
Db 758 --EDGRYFNG--QDQPCHRFCATCAGADGCINCTEGYEMD 797

RESULT 7

JC6148
subtilisin-like proteolysin convertase (EC 3.4.21.-) homolog - human
N/Alternate names: PC6A (protease)
C/Species: Homo sapiens (man)
C/Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 22-Jun-1999
C/Accession: JC6148
R:Miranda, L.; Wolf, J.; Pichantes, S.; Duke, R.; Franzusoff, A.
Proc. Natl. Acad. Sci. U.S.A. 93, 7695-7700, 1996
A/Title: Isolation of the human PC6 gene encoding the putative host protease for HIV-1
A/Reference number: JC6148; MUID:96353880; PMID:8755538
A/Contents: CEM T-cell
A/Accession: JC6148
A/Molecule type: mRNA
A/Residues: 1-915 <MR>
A/Cross-references: GB:56387; NID:g1498312; PIDN:AAC50643.1; PID:g1498313
C/Comment: This protein functions as a soluble enzyme within the secretory pathway. It is
C/Genetics:
A/Status: PCS
C/Superfamily: subtilisin-like protease PACE4; subtilisin homology
C/Keywords: glycoprotein, hydrolase, serine proteinase
F:144-402/Domain: subtilisin homology <SBT>

Query Match 9.1%; Score 82.5; DB 2; Length 915;
Best Local Similarity 26.0%; Pred. No. 14;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;

QY 27 TGVAMRSCPEBQYWDPLIGTCMCKTICNHOSQRTCAAF-----CR-----SLSC 71
Db 719 TNSCVTHCPDGSYQDTKKNLCRKSENC-----KTCTEFHNCTECRDGLSLQSRCSVSC 773

QY 72 RKEGKPYDHLRDCISCSAIC-----GQHPKQC-----AYCEN 106
Db 774 --EDGRYFNG--QDQPCHRFCATCAGADGCINCTEGYEMD 813

RESULT 8

152527
PACE4A - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Jul-1999
C/Accession: 152527
R:Hosaka, M.; Murakami, K.; Nakayama, K.
Biomed. Res. 15, 383-390, 1994
A/Title: PACE4A is a ubiquitous endoprotease that has similar but not identical substrates
A/Reference number: 152527
A/Accession: 152527
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-932 <RES>
A/Cross-references: GB:D50060; NID:g769700; PIDN:BA08777.1; PID:g769701
C/Superfamily: subtilisin-like protease PACE4; subtilisin homology
F:112-410/Domain: subtilisin homology <SBT>

Query Match 9.0%; Score 82; DB 2; Length 932;
Best Local Similarity 25.0%; Pred. No. 16;
Matches 28; Conservative 16; Mismatches 44; Indels 24; Gaps 5;

QY 16 DQERFPGILMTGVAMRSCPEBQYWDPLIGTCMCK--TICNHOSQRTCAAFCSLSCK 73
Db 650 DEER-----YTGVCHEPCGDKGCDGNADQCLNCHFLSNGSKTNKCVSECE----- 696

QY 74 EOGKPYDHLRDCISCSAIC-----GQHPKQC-----AYCENKLRSPYNLPP 116
Db 697 PLGYFGMAARCRCHKGCCTGTGRSPAQCLSGRGFYHHQETNVTCLCP 748

RESULT 9

S53457
dominant autoantigen gp 330 - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 18-Aug-2000
C/Accession: S53457
R:Jokhadze, G.G.; Oleinikov, A.V.; Kanalas, J.J.; Makker, S.P.
Biochem. J. 305, 711-713, 1995
A/Title: Different molecular forms of rat kidney gp330, the dominant autoantigen of active
A/Reference number: S53457; MUID:95151000; PMID:7848267
A/Accession: S53457
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-1650 <OK>
C/Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding
F:29-65/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F:72-106/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F:111-147/Domain: EGF homology <EG1>
F:153-188/Domain: EGF homology <EG2>
F:196-235/Domain: LDL receptor WYTD-containing repeat homology <YW01>
F:236-278/Domain: LDL receptor WYTD-containing repeat homology <YW02>
F:279-329/Domain: LDL receptor WYTD-containing repeat homology <YW03>
F:330-373/Domain: LDL receptor WYTD-containing repeat homology <YW04>
F:374-414/Domain: LDL receptor WYTD-containing repeat homology <YW05>
F:415-457/Domain: LDL receptor WYTD-containing repeat homology <YW06>
F:466-505/Domain: EGF homology <EG3>
F:509-545/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F:550-586/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F:595-631/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F:636-672/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F:679-715/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F:720-755/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F:760-794/Domain: LDL receptor ligand-binding repeat homology <LDL8>
F:799-833/Domain: LDL receptor ligand-binding repeat homology <LDL9>
F:843-879/Domain: LDL receptor ligand-binding repeat homology <LDL10>
F:884-921/Domain: LDL receptor ligand-binding repeat homology <LDL11>
F:929-963/Domain: LDL receptor ligand-binding repeat homology <LDL12>
F:971-1006/Domain: EGF homology <EG4>
F:1012-1048/Domain: EGF homology <EG5>
F:1055-1099/Domain: LDL receptor WYTD-containing repeat homology #status atypical <YW07>

A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
 C;Superfamily: protein-tyrosine kinase, receptor type tie; EGF homology; fibronectin ty
 C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phospho
 F;1-22/Domain: signal sequence #status predicted <SIG>
 F;23-124/Domain: product: protein-tyrosine kinase, receptor type tek #status predicted <MAT>
 F;37-104/Domain: immunoglobulin homology <IM>
 F;115-137/Region: cell attachment (R-G-D) motif
 F;211-251/Domain: EGF homology <EG1>
 F;255-298/Domain: EGF homology <EG2>
 F;302-340/Domain: EGF homology <EG3>
 F;364-426/Domain: immunoglobulin homology <IM2>
 F;447-527/Domain: fibronectin type III repeat homology <FN3A>
 F;542-625/Domain: fibronectin type III repeat homology <FN3B>
 F;638-720/Domain: fibronectin type III repeat homology <FN3C>
 F;752-772/Domain: transmembrane #status predicted <TM>
 F;822-1099/Domain: protein kinase homology <KIN>
 F;830-838/Region: protein kinase ATP-binding motif
 F;140,158,399,438,464,560,566,649,691/Binding site: carbohydrate (Asn) (covalent) #statu
 F;855,872,964/Active site: Lys, Glu, Asp #status predicted

Query Match 8.9%; Score 81; DB 1; Length 1124;
 Best Local Similarity 24.2%; Pred. No. 22;
 Matches 39; Conservative 15; Mismatches 63; Indels 44; Gaps 8;

Qy 26 WTGVAMRSCPEBQKWP---LLGTCM-----SKTTICN-HQSQ 59
 Db 203 FTPLIVRRC-BAQKGPFCNHLCTACMNNVCHBDTGECIPFGMGRTCEKACELHTFG 261

Qy 60 RTCAAFCSLSCKEKGKFDHLRDCISCASTCGQHCKQCAFENKLRSPVNLPELR 119
 Db 262 RTCKERCSCG---DEGCSYVFCPLDPYGCSCATGKGLQCNCAECH---FGFYGPCK 312

Qy 120 RQSGEVENNSDNRGRYOGLERHGEASPALPGLKLSADQV 160
 Db 313 LRCSG---NNGEMCDRFG---GCLCSFGWGLQCCERGI 345

RESULT 13

153282
 gene PACE4 protein - rat

C;Species: Rattus norvegicus (Norway rat)
 C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 22-Jun-1999
 C;Accession: 153282
 R;Johnson, R.C.; Darlington, D.N.; Hand, T.A.; Bloomquist, B.T.; Mains, R.E.
 Endocrinology 135, 1178-1185, 1994
 A;Title: PACE4, a subtilisin-like endoprotease prevalent in the anterior pituitary and
 A;Reference number: 153282; MUID:94349873; PMID:8070361
 A;Accession: 153282
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-937 <RES>
 A;Cross-references: GB:U31894; NID:9496221; PIDN:AAA61987.1; PID:9496222
 C;Genetic8:
 A;Gene: PACE4
 C;Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
 F;177-415/Domain: subtilisin homology <SBT>

Query Match 8.9%; Score 80.5; DB 2; Length 937;
 Best Local Similarity 24.1%; Pred. No. 21;
 Matches 27; Conservative 17; Mismatches 45; Indels 23; Gaps 5;

Qy 16 DOEERFQGLWTGVAMRSCPEBQWMDPLLTGTCMCK--TICNHSQRTCAAFCSLSCKR 73
 Db 654 EEEERY-----TGCHPCGDKGCGPSADQCLNCVHFSLSKSKTRKCVSIC----- 701

Qy 74 EOGKFDYDHLRDCISCASTC---GQHPKQC---AFCEKLRSPVNLPP 116
 Db 702 PLGYGDPAARCRCHKGCETCTGRSPFGQCLSCRRGFYHDETNVTVLCP 753

RESULT 14
 H69834
 hypothetical protein yhjQ - Bacillus subtilis

C;Species: Bacillus subtilis
 C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
 C;Accession: H69834

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero
 C.; Bron, S.; Brulliet, S.; Brusch, C.V.; Caldwell, B.; Capuani, V.; Carter, N.M.; Cho
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
 Nature 390, 249-256, 1997
 A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc
 lech, J.; Harwood, C.R.; Henauf, A.; Hilbert, H.; Holtsappel, S.; Hosono, S.; Hullo, M.F.
 Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
 A;Authors: Lamber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
 Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon
 A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Toigoni, A.; Tosato, V.; Uchiyama
 T.; Wintere, P.; Wipac, A.; Yamamoto, H.; Yamano, K.; Yasumoto, K.; Yata, K.; Yoshida, K
 A;Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
 A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A;Reference number: A69580; MUID:98044033; PMID:9384377
 A;Accession: H69834
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-108 <KIN>
 A;Cross-references: GB:299109; GB:AL009126; NID:92633260; PIDN:CAB12900.1; PID:el183062;
 A;Experimental source: strain 168
 C;Genetics:
 A;Gene: yhjQ

Query Match 8.8%; Score 80; DB 2; Length 108;
 Best Local Similarity 23.6%; Pred. No. 3.5;
 Matches 25; Conservative 9; Mismatches 26; Indels 46; Gaps 5;

Qy 37 EOYMDPLGTGTCMCKTTICN-----QSORTCA----- 63
 Db 2 EOYSACIEACIDCKKACNHCFTKCLBSVOHLSGCRRLRBCADTICALAVKAMQTSF 61

Qy 64 -----AFCRSL--SCRKQKGF-YDHLRDCISCASTCGQHCKQ 100
 Db 62 FMRKICALCADICEACGTGCKHDDH----CQACAKACFTCAEGC 103

RESULT 15

125169
 hypothetical protein T23F1.6 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
 C;Accession: T25169
 R;Wilkinson, J.
 submitted to the EMBL Data Library, October 1996
 A;Reference number: 219990
 A;Accession: T25169
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-330 <WIL>
 A;Cross-references: EMBL:T281129; PIDN:CAB03405.1; GSPDB:GN00023; CESP:T23F1.6
 A;Experimental source: clone T23F1
 C;Genetics:
 A;Gene: CESP:T23F1.6
 A;Map position: 5
 A;Introns: 16/3
 C;Superfamily: gliadin

Query Match 8.8%; Score 80; DB 2; Length 330;
 Best Local Similarity 24.6%; Pred. No. 9.4;
 Matches 33; Conservative 14; Mismatches 55; Indels 32; Gaps 8;

Qy 33 SCPEBQWMDPLLTGTCM-----SKTTIC-----NHQSORTCAAFCSLSCKRQG---KEYD 80
 Db 58 SCASSQYQQLQTSQCMPCAGQSCSQGCSQNTNTQCPCTQGSQCSGCMPTSTPIPSAQ 117

Qy 81 HLKDCIS-CASTCGH--PQCAVFCENKLRSPVNLPELRQSGE---VENNSD-- 131
 Db 118 SCLPCECENKMQOCTQOQTAQCCPITCOQC-----QDCGSGTGMNMYNQDPY 166

Oy 132 NSGRYQLEHRSSE 145
| : | : | :
Db 167 NQMYGGYNQGNQ 180

Search completed: February 4, 2003, 12:59:52
Job time : 26.4899 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 4, 2003, 12:56:41 ; Search time 7.54251 Seconds
(without alignments)
315.977 Million cell updates/sec

Title: US-09-854-864-13

Perfect score: 498

Sequence: 1 CSONEHYPSILHACIPQQLR.....SEYFDSILHACPPATCPYC 81

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 93 | 18.7 | 166 | 2 | US-08-810-572A-6 |
| 2 | 93 | 18.7 | 166 | 4 | US-09-290-333-6 |
| 3 | 93 | 18.7 | 293 | 4 | US-08-810-572A-2 |
| 4 | 93 | 18.7 | 293 | 4 | US-09-290-333-2 |
| 5 | 82 | 16.5 | 508 | 4 | US-09-019-095A-8 |
| 6 | 82 | 16.5 | 521 | 4 | US-09-019-095A-2 |
| 7 | 82 | 16.5 | 526 | 4 | US-09-019-095A-2 |
| 8 | 80 | 16.1 | 3075 | 2 | US-08-460-309-5 |
| 9 | 80 | 16.1 | 3075 | 2 | US-08-125-077-5 |
| 10 | 80 | 16.1 | 5405 | 4 | US-08-718-388-9 |
| 11 | 79 | 15.9 | 320 | 4 | US-09-183-861-22 |
| 12 | 79 | 15.9 | 320 | 4 | US-09-183-861-55 |
| 13 | 79 | 15.9 | 320 | 4 | US-09-022-765-22 |
| 14 | 79 | 15.9 | 320 | 4 | US-09-022-765-22 |
| 15 | 79 | 15.9 | 545 | 4 | US-09-022-765-55 |
| 16 | 78 | 15.7 | 109 | 2 | US-08-527-044-2 |
| 17 | 78 | 15.7 | 109 | 2 | US-09-013-780-2 |
| 18 | 77.5 | 15.6 | 139 | 3 | US-08-965-903B-20 |
| 19 | 77.5 | 15.6 | 139 | 3 | US-09-370-338-4 |
| 20 | 76.5 | 15.4 | 2414 | 1 | US-08-227-536-2 |
| 21 | 76.5 | 15.4 | 2414 | 1 | PCT-US95-04682-2 |
| 22 | 76 | 15.3 | 2441 | 1 | US-08-194-468-2 |
| 23 | 76 | 15.3 | 2441 | 3 | US-08-961-739-2 |
| 24 | 76 | 15.3 | 2441 | 4 | US-09-514-247A-8 |
| 25 | 76 | 15.3 | 2442 | 4 | US-09-514-247A-10 |
| 26 | 75.5 | 15.2 | 156 | 3 | US-08-600-982-30 |
| 27 | 75.5 | 15.2 | 156 | 5 | PCT-US94-10261A-30 |

| | | | | | | |
|----|------|------|------|---|--------------------|-------------------|
| 28 | 75.5 | 15.2 | 1713 | 3 | US-08-600-982-24 | Sequence 24, Appl |
| 29 | 75.5 | 15.2 | 1713 | 5 | PCT-US94-10261A-24 | Sequence 24, Appl |
| 30 | 75 | 15.1 | 219 | 1 | US-08-152-019A-31 | Sequence 31, Appl |
| 31 | 75 | 15.1 | 219 | 2 | US-08-460-309-18 | Sequence 18, Appl |
| 32 | 75 | 15.1 | 219 | 2 | US-08-125-077-18 | Sequence 18, Appl |
| 33 | 75 | 15.1 | 430 | 3 | US-08-997-897-2 | Sequence 2, Appl |
| 34 | 75 | 15.1 | 430 | 4 | US-09-156-836B-2 | Sequence 2, Appl |
| 35 | 73.5 | 14.8 | 435 | 4 | US-09-561-989-10 | Sequence 10, Appl |
| 36 | 73 | 14.7 | 689 | 4 | US-09-177-249-2 | Sequence 2, Appl |
| 37 | 73 | 14.7 | 689 | 4 | US-09-061-769A-2 | Sequence 2, Appl |
| 38 | 72.5 | 14.6 | 969 | 2 | US-08-284-941-2 | Sequence 2, Appl |
| 39 | 72.5 | 14.6 | 969 | 2 | US-08-447-642-2 | Sequence 2, Appl |
| 40 | 72.5 | 14.6 | 969 | 4 | US-09-236-503-2 | Sequence 2, Appl |
| 41 | 72.5 | 14.6 | 969 | 5 | PCT-US93-02147A-2 | Sequence 2, Appl |
| 42 | 72 | 14.5 | 275 | 1 | US-08-312-870-7 | Sequence 7, Appl |
| 43 | 72 | 14.5 | 366 | 4 | US-08-857-076-103 | Sequence 103, App |
| 44 | 72 | 14.5 | 446 | 1 | US-08-307-444A-5 | Sequence 5, Appl |
| 45 | 72 | 14.5 | 446 | 1 | US-08-587-389-5 | Sequence 5, Appl |

ALIGNMENTS

RESULT 1
US-08-810-572A-6
Sequence 6, Application US/08810572A
Patent No. 5969102
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
TITLE OF INVENTION: A LYMPOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
TITLE OF INVENTION: THEROF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,572A
FILING DATE: 28-FEB-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-810-572A-6
Query Match 18.7%; Score 93; DB 2; Length 166;
Best local Similarity 28.4%; Pred. No. 0.037;


```

; ADDRESS: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; FLOOR
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/290,333
; FILING DATE: 12-Apr-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-290-333-2
;
Query Match      18.7%; Score 93; DB 4; Length 293;
Best Local Similarity 28.4%; Pred. No. 0.064;
Matches 21; Conservative 13; Mismatches 22; Indels 18; Gaps 5;
;
Qy 1 CSQNYFDSLHACIPQRCSSNTPPLTCQRYC---C-----EYFDSLHACPCLRS 51
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 34 CPEQYWDMLCTCMSCKTKCNHQS-QRTCAAFCSLSCKEQGKYDHLR--DCISCA 90
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 52 -----PPTCYCC 59
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 91 SICGHPKQCAVFC 104
;
RESULT 5
US-09-019-095A-8
; Sequence 8, Application US/09019095A
; Patent No. 6287858
; GENERAL INFORMATION:
; APPLICANT: D'Andrea, Alan D.
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: Deubiquitinating Enzymes That Regulate
; TITLE OF INVENTION: Cell Growth
; FILE REFERENCE: DPCI-435D2A2
; CURRENT APPLICATION NUMBER: US/09/019,095A
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: PCT/US96/12884
; PRIOR FILING DATE: 1996-08-07
; PRIOR APPLICATION NUMBER: US 60/002,066
; PRIOR FILING DATE: 1995-08-09
; PRIOR APPLICATION NUMBER: US 60/019,787
; PRIOR FILING DATE: 1996-06-14
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Murine
;
; ORGANISM: Murine
US-09-019-095A-8
;
Query Match      16.5%; Score 82; DB 4; Length 508;
Best Local Similarity 35.8%; Pred. No. 1.2;
Matches 19; Conservative 8; Mismatches 18; Indels 8; Gaps 2;
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Qy 19 LRCSSNTPPLTCQRYCEYFDSLHACPCLRCSPPTCYCCFHSYFDSLHA 71
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 55 LQCLHTHTPPL-----ADYMLSQEHSQTC--CSFGCKLCAMEALVTSLLHS 99
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
;
RESULT 6
US-09-019-095A-22
; Sequence 22, Application US/09019095A
; Patent No. 6287858
; GENERAL INFORMATION:
; APPLICANT: D'Andrea, Alan D.
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: Deubiquitinating Enzymes That Regulate
; TITLE OF INVENTION: Cell Growth
; FILE REFERENCE: DPCI-435D2A2
; CURRENT APPLICATION NUMBER: US/09/019,095A
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: PCT/US96/12884
; PRIOR FILING DATE: 1996-08-07
; PRIOR APPLICATION NUMBER: US 60/002,066
; PRIOR FILING DATE: 1995-08-09
; PRIOR APPLICATION NUMBER: US 60/019,787
; PRIOR FILING DATE: 1996-06-14
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Murine
US-09-019-095A-22
;
Query Match      16.5%; Score 82; DB 4; Length 521;
Best Local Similarity 35.8%; Pred. No. 1.2;
Matches 19; Conservative 8; Mismatches 18; Indels 8; Gaps 2;
;
Qy 19 LRCSSNTPPLTCQRYCEYFDSLHACPCLRCSPPTCYCCFHSYFDSLHA 71
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 61 LQCLHTHTPPL-----ADYMLSQEHSQTC--CSFGCKLCAMEALVTSLLHS 105
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
;
RESULT 7
US-09-019-095A-2
; Sequence 2, Application US/09019095A
; Patent No. 6287858
; GENERAL INFORMATION:
; APPLICANT: D'Andrea, Alan D.
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: Deubiquitinating Enzymes That Regulate
; TITLE OF INVENTION: Cell Growth
; FILE REFERENCE: DPCI-435D2A2
; CURRENT APPLICATION NUMBER: US/09/019,095A
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: PCT/US96/12884
; PRIOR FILING DATE: 1996-08-07
; PRIOR APPLICATION NUMBER: US 60/002,066
; PRIOR FILING DATE: 1995-08-09
; PRIOR APPLICATION NUMBER: US 60/019,787
; PRIOR FILING DATE: 1996-06-14
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 526
; TYPE: PRT
; ORGANISM: Murine
US-09-019-095A-2
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Query Match 16.5%; Score 82; DB 4; Length 526;
Best Local Similarity 35.8%; Pred. No. 1.2;
Matches 19; Conservative 8; Mismatches 18; Indels 8; Gaps 2;

QY 19 LRCSNTPPTCCRYCEYFDSLHACPCRCSPPTCCYCCFSEYDLSLHA 71
DB 66 LQCLTHPLPPL-----ADYMLSQEHSGTC--CSPECKLCAEMALVTQSILHS 110

RESULT 8

US-08-460-309-5
Sequence 5, Application US/08460309
Patent No. 5837496
GENERAL INFORMATION:
APPLICANT: Engvall, Eva
APPLICANT: Leivo, Ilmo
TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
TITLE OF INVENTION: Fragments and Uses Thereof
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,309
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/125,077
FILING DATE: 22-SEP-1993
APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9721
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3075 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-460-309-5

Query Match 16.1%; Score 80; DB 2; Length 3075;
Best Local Similarity 23.4%; Pred. No. 10;
Matches 29; Conservative 10; Mismatches 37; Indels 48; Gaps 8;

QY 1 CSQNEFYFDSL--HACIPCO-----LRCSNTPPTCCRYCCF-- 36
DB 831 CADGYGNFTVPBESCVPCDCSGNVDPSEAGHCDVTEGCLKLGANTDGAHCR--CADGF 889
QY 37 YPDSL-----LHACPC-----LRCSNTPPTCCRYCCF-- 73
DB 890 YGDAYTAKKRCRACGCHVAGSHSAVCHLETGLDCKPKNVTTGQCCDGLHGYGLDSGHCR 949
QY 74 PATC 77

DB 950 PCNC 953

RESULT 9

US-08-125-077-5
Sequence 5, Application US/08125077
Patent No. 5872231
GENERAL INFORMATION:
APPLICANT: Engvall, Eva
APPLICANT: Leivo, Ilmo
TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
TITLE OF INVENTION: Fragments and Uses Thereof
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,077
FILING DATE: 22-SEP-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9721
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3075 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-125-077-5

Query Match 16.1%; Score 80; DB 2; Length 3075;
Best Local Similarity 23.4%; Pred. No. 10;
Matches 29; Conservative 10; Mismatches 37; Indels 48; Gaps 8;

QY 1 CSQNEFYFDSL--HACIPCO-----LRCSNTPPTCCRYCCF-- 36
DB 831 CADGYGNFTVPBESCVPCDCSGNVDPSEAGHCDVTEGCLKLGANTDGAHCR--CADGF 889
QY 37 YPDSL-----LHACPC-----LRCSNTPPTCCRYCCF-- 73
DB 890 YGDAYTAKKRCRACGCHVAGSHSAVCHLETGLDCKPKNVTTGQCCDGLHGYGLDSGHCR 949
QY 74 PATC 77
DB 950 PCNC 953

RESULT 10
US-08-718-388-9

Sequence 9, Application US/08718388
Patent No. 6271362
GENERAL INFORMATION
APPLICANT: MORIKAWA, MINORU
APPLICANT: HARADA, NAOKI
TITLE OF INVENTION: GENE ENCODING IGG FC REGION-BINDING
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,388
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 0230-111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 5405 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-718-388-9

Query Match 16.1%; Score 80; DB 4; Length 5405;
Best Local Similarity 25.4%; Pred. No. 17;
Matches 29; Conservative 12; Mismatches 25; Indels 48; Gaps 10;

Qy 1 CSQNEVPSILHACT-PCQLRCSNTPPLTCQYCCCEVPSILHACPC-----LRCS 51
Db 2733 CPQNGHYE---LCADTCSLGSALSAPLQCPDGCAR-----GQCDSGRLVNGQACV 2781
Qy 52 PPTCYC-CFHS-BYFD---SLI-----HACPPA-TQCP 79
Db 2782 P--10QCGCYHNGAYVEPQVTLIDNCROQCTCHAGKVVVCOEHSCKPQVQCP 2833

RESULT 11
US-09-183-861-22
Sequence 22, Application US/09183861
Patent No. 6365165
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USEIN THE THERAPY AND
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/183,861
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/022,765
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-183-861-22

Query Match 15.9%; Score 79; DB 4; Length 320;
Best Local Similarity 27.5%; Pred. No. 15;
Matches 25; Conservative 11; Mismatches 23; Indels 32; Gaps 7;

Qy 13 ACIPQ-----LRCSN---TPPLTCQYCCCEVPSILHACPLRCSPT- 54
Db 105 ACVRCQBNCFSCDSKANKQCAPNVYLITLITCSPVAC---NIEH---CMQCDPQT 157
Qy 55 --COYCC--FHSEVPSLH---ACPPATQ 78
Db 158 SRCQCVSPYVVDYDGLCRISDACSPVNC 188

RESULT 12
US-09-183-861-55
Sequence 55, Application US/09183861
Patent No. 6365165
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USEIN THE THERAPY AND
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/183,861
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/022,765
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C3

```
TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 55:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 320 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FRAGMENT TYPE: internal
US-09-183-861-55
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Query Match 15.9%; Score 79; DB 4; Length 320;
Best Local Similarity 27.5%; Pred. No. 1.5;
Matches 25; Conservative 11; Mismatches 23; Indels 32; Gaps 7;
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QY 13 ACIPQ-----LRCSN---TPPLTCQRYCCEYFDSLHLACPLRCSPPT- 54
DB 105 ACVRCQEPNCFSCDSANKCTQCAPNYVLTPLTCSPVAC---NIEH---CMQCDPQTP 157
QY 55 --COYCC--FHSEYFDSLH---ACPPATCQ 78
DB 158 SRCQECVSPYVDSYDGLCRSLDACSVPNCK 188
```

```
RESULT 13
US-09-022-765-22
/ Sequence 22, Application US/09022765
/ Patent No. 6375955
/ GENERAL INFORMATION:
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Campos-Neto, Antonio
/ APPLICANT: Webb, John R.
/ APPLICANT: Dillon, David C.
/ APPLICANT: Skeiky, Yaser A.W.
/ TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE THERAPY AND
/ NUMBER OF SEQUENCES: 87
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: SEED and BERRY LLP
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: USA
/ ZIP: 98104-7092
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/022,765
/ FILING DATE: 12-FEB-1998
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Makl, David J.
/ REGISTRATION NUMBER: 31,392
/ REFERENCE/DOCKET NUMBER: 210121.420C3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 22:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 320 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FRAGMENT TYPE: internal
US-09-022-765-22
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Query Match 15.9%; Score 79; DB 4; Length 320;
Best Local Similarity 27.5%; Pred. No. 1.5;
Matches 25; Conservative 11; Mismatches 23; Indels 32; Gaps 7;
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QY 13 ACIPQ-----LRCSN---TPPLTCQRYCCEYFDSLHLACPLRCSPPT- 54
DB 105 ACVRCQEPNCFSCDSANKCTQCAPNYVLTPLTCSPVAC---NIEH---CMQCDPQTP 157
QY 55 --COYCC--FHSEYFDSLH---ACPPATCQ 78
DB 158 SRCQECVSPYVDSYDGLCRSLDACSVPNCK 188
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RESULT 14
US-09-022-765-55
/ Sequence 55, Application US/09022765
/ Patent No. 6375955
/ GENERAL INFORMATION:
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Campos-Neto, Antonio
/ APPLICANT: Webb, John R.
/ APPLICANT: Dillon, David C.
/ APPLICANT: Skeiky, Yaser A.W.
/ TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE THERAPY AND
/ NUMBER OF SEQUENCES: 87
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: SEED and BERRY LLP
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: USA
/ ZIP: 98104-7092
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/022,765
/ FILING DATE: 12-FEB-1998
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Makl, David J.
/ REGISTRATION NUMBER: 31,392
/ REFERENCE/DOCKET NUMBER: 210121.420C3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 55:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 320 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FRAGMENT TYPE: internal
US-09-022-765-55
```

```
Query Match 15.9%; Score 79; DB 4; Length 320;
Best Local Similarity 27.5%; Pred. No. 1.5;
Matches 25; Conservative 11; Mismatches 23; Indels 32; Gaps 7;
```

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QY 13 ACIPQ-----LRCSN---TPPLTCQRYCCEYFDSLHLACPLRCSPPT- 54
DB 105 ACVRCQEPNCFSCDSANKCTQCAPNYVLTPLTCSPVAC---NIEH---CMQCDPQTP 157
QY 55 --COYCC--FHSEYFDSLH---ACPPATCQ 78
DB 158 SRCQECVSPYVDSYDGLCRSLDACSVPNCK 188
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```
RESULT 15
US-09-019-095A-38
/ Sequence 38, Application US/09019095A
/ Patent No. 6287858
/ GENERAL INFORMATION:
/ APPLICANT: D'Andrea, Alan D.
```

Sat Feb 8 14:52:27 2003

us-09-854-864-13.rai

Page 7

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1  APPLICANT: Zhu, Yuan      Deubiquitinating Enzymes That Regulate
2  TITLE OF INVENTION:
3  TITLE OF INVENTION: Cell Growth
4  FILE REFERENCE: DPCI-435p22
5  CURRENT APPLICATION NUMBER: US/09/019,095A
6  CURRENT FILING DATE: 1998-02-05
7  PRIOR APPLICATION NUMBER: PCT/US96/12884
8  PRIOR FILING DATE: 1996-08-07
9  PRIOR APPLICATION NUMBER: US 60/002,066
10 PRIOR FILING DATE: 1995-08-09
11 PRIOR APPLICATION NUMBER: US 60/019,787
12 PRIOR FILING DATE: 1996-06-14
13 NUMBER OF SEQ ID NOS: 51
14 SOFTWARE: FastSeq for Windows Version 3.0
15 SEQ ID NO 38
16 LENGTH: 545
17 TYPE: PRT
18 ORGANISM: murine
19 US-09-019-095A-38

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| Query Match | 15.9% | Score 79; | DB 4; | Length 545; |
| Best Local Similarity | 34.0% | Pred. No. 2.4; | | |
| Matches 18; | Conservative 9; | Mismatches 18; | Indels 8; | Gaps 2; |

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Db 66 LQCLTHTPL-----ADYMLSQEYSQTC--CSPEGCKACMEAHYQSLHS 110

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Search completed: February 4, 2003, 13:00:15
Job time : 10.5425 secs
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Page 7

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 4, 2003, 12:59:16 ; Search time 5.24696 Seconds
(without alignments)
342.239 Million cell updates/sec

Title: US-09-854-864-13

Perfect score: 498
Sequence: 1 CSONEYFDSLHACIPQCLR.....SEYFDSLHACPPATCPYC 81

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 129505 seqs, 22169297 residues

Total number of hits satisfying chosen parameters: 129505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|---------------------|-------------------|
| 1 | 498 | 100.0 | 81 | 10 US-09-854-864-13 | Sequence 13, Appl |
| 2 | 230.5 | 46.3 | 207 | 9 US-10-077-438-3 | Sequence 3, Appl |
| 3 | 230.5 | 46.3 | 207 | 9 US-10-077-137-3 | Sequence 3, Appl |
| 4 | 201.5 | 40.5 | 283 | 10 US-09-854-864-9 | Sequence 9, Appl |
| 5 | 201 | 40.4 | 34 | 10 US-09-854-864-7 | Sequence 7, Appl |
| 6 | 201 | 40.4 | 51 | 10 US-09-854-864-6 | Sequence 6, Appl |
| 7 | 201 | 40.4 | 58 | 10 US-09-854-864-21 | Sequence 21, Appl |
| 8 | 201 | 40.4 | 181 | 10 US-09-854-864-5 | Sequence 5, Appl |
| 9 | 201 | 40.4 | 184 | 9 US-10-077-438-1 | Sequence 1, Appl |
| 10 | 201 | 40.4 | 184 | 9 US-10-077-438-7 | Sequence 7, Appl |
| 11 | 201 | 40.4 | 184 | 9 US-10-077-137-1 | Sequence 1, Appl |
| 12 | 201 | 40.4 | 184 | 9 US-10-077-137-7 | Sequence 7, Appl |
| 13 | 201 | 40.4 | 184 | 9 US-10-068-725-2 | Sequence 2, Appl |
| 14 | 153 | 30.7 | 117 | 10 US-09-854-864-12 | Sequence 12, Appl |
| 15 | 139.5 | 28.0 | 281 | 10 US-09-854-864-10 | Sequence 10, Appl |
| 16 | 136 | 27.3 | 185 | 10 US-09-854-864-11 | Sequence 11, Appl |
| 17 | 105 | 21.1 | 67 | 10 US-09-854-864-16 | Sequence 16, Appl |
| 18 | 93 | 18.7 | 166 | 10 US-09-854-864-15 | Sequence 15, Appl |
| 19 | 93 | 18.7 | 291 | 9 US-09-779-050A-43 | Sequence 43, Appl |

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| 20 | 93 | 18.7 | 293 | 9 US-09-779-050A-42 | Sequence 42, Appl |
| 21 | 93 | 18.7 | 293 | 9 US-10-084-971-2 | Sequence 2, Appl |
| 22 | 93 | 18.7 | 293 | 9 US-10-068-725-4 | Sequence 4, Appl |
| 23 | 93 | 18.7 | 293 | 9 US-09-302-863-2 | Sequence 2, Appl |
| 24 | 93 | 18.7 | 293 | 10 US-09-879-919-22 | Sequence 22, Appl |
| 25 | 93 | 18.7 | 293 | 10 US-09-854-864-14 | Sequence 14, Appl |
| 26 | 93 | 18.7 | 293 | 10 US-09-961-376-2 | Sequence 2, Appl |
| 27 | 93 | 18.7 | 293 | 10 US-09-854-864-18 | Sequence 18, Appl |
| 28 | 91.5 | 18.4 | 231 | 10 US-09-864-761-37946 | Sequence 37946, A |
| 29 | 89.5 | 18.0 | 134 | 10 US-09-864-761-39564 | Sequence 39564, A |
| 30 | 84.5 | 17.0 | 270 | 10 US-09-764-855-145 | Sequence 145, App |
| 31 | 83 | 16.7 | 93 | 10 US-09-864-761-46675 | Sequence 46675, A |
| 32 | 82 | 16.5 | 230 | 10 US-09-874-062-3 | Sequence 8, Appl |
| 33 | 81 | 16.3 | 241 | 9 US-10-084-594-8 | Sequence 10, Appl |
| 34 | 81 | 16.3 | 1587 | 10 US-09-845-583-10 | Sequence 39864, A |
| 35 | 80.5 | 16.2 | 85 | 10 US-09-864-761-39864 | Sequence 9, Appl |
| 36 | 80.5 | 16.2 | 1798 | 10 US-09-938-275-5 | Sequence 5, Appl |
| 37 | 80 | 16.1 | 3075 | 10 US-09-938-275-5 | Sequence 5, Appl |
| 38 | 80 | 16.1 | 5405 | 9 US-10-025-380-1116 | Sequence 1116, Ap |
| 39 | 80 | 16.1 | 5405 | 10 US-09-922-217-1116 | Sequence 20, Appl |
| 40 | 79 | 15.9 | 59 | 10 US-09-854-864-20 | Sequence 22, Appl |
| 41 | 79 | 15.9 | 320 | 9 US-09-991-496-55 | Sequence 55, Appl |
| 42 | 79 | 15.9 | 320 | 9 US-09-991-496-55 | Sequence 55, Appl |
| 43 | 79 | 15.9 | 320 | 10 US-09-874-923-22 | Sequence 22, Appl |
| 44 | 79 | 15.9 | 320 | 10 US-09-874-923-55 | Sequence 55, Appl |
| 45 | 79 | 15.9 | 709 | 9 US-09-991-496-121 | Sequence 121, App |

ALIGNMENTS

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RESULT 1
US-09-854-864-13
; Sequence 13, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLVS/AP-3, AND TACI
; FILE REFERENCE: A-6868
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
; US-09-854-864-13

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Best Local Similarity 100.0%; Pred. No. 1.6e-35;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CSONEYFDSLHACIPQCLRCSNTPTLCORCCYCEYDSLHACPCURCSPPTCQYCCF 60
DB      1 CSONEYFDSLHACIPQCLRCSNTPTLCORCCYCEYDSLHACPCURCSPPTCQYCCF 60
QY      61 HSEYFDSLHACPPATCPYC 81
DB      61 HSEYFDSLHACPPATCPYC 81

RESULT 2
US-10-077-438-3
; Sequence 3, Application US/10077438
; Patent No. US20020165156A1
; GENERAL INFORMATION:
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; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Techopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-3

Query Match          46.3%; Score 230.5; DB 9; Length 207;
Best Local Similarity 57.8%; Pred. No. 6.4e-13;
Matches 48; Conservative 0; Mismatches 4; Indels 31; Gaps 4;
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Qy 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYCCEYFDSLHAC-PC-LRCSPPTCQYC 58
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Db 46 CSQNEYPDSLHACIPCOLRCSSNTPPLTC-----LHACIPCOLRCSSNT----- 90
Qy 59 CPHSEYFDSLHACPPATCQPYC 81
    |||||
Db 91 -----PPLTCQRYC 99
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RESULT 3
US-10-077-137-3
; Sequence 3, Application US/10077137
; Patent No. US2002017267A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Techopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-3
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Query Match 46.3%; Score 230.5; DB 9; Length 207;

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Best Local Similarity 57.8%; Pred. No. 6.4e-13;
Matches 48; Conservative 0; Mismatches 4; Indels 31; Gaps 4;

Qy 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYCCEYFDSLHAC-PC-LRCSPPTCQYC 58
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Db 91 -----PPLTCQRYC 99
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RESULT 4
US-09-854-864-9
; Sequence 9, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-9

Query Match          40.5%; Score 201.5; DB 10; Length 283;
Best Local Similarity 60.6%; Pred. No. 2.1e-10;
Matches 40; Conservative 2; Mismatches 9; Indels 15; Gaps 3;
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Qy 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYCCEYFDSL-----LHACPC 47
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Db 5 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYCNASTVNSKGTNAGGGGDKTHTCP- 63
Qy 48 LRCSP 53
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Db 64 -PCPAP 68
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RESULT 5
US-09-854-864-7
; Sequence 7, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-7
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Query Match 40.4%; Score 201; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 4e-11;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 34

RESULT 6

US-09-854-864-6
; Sequence 6, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-6

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Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 5 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 38

RESULT 7

US-09-854-864-21
; Sequence 21, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-21

Query Match 40.4%; Score 201; DB 10; Length 58;
Best Local Similarity 100.0%; Pred. No. 6.3e-11;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 34

RESULT 8
US-09-854-864-5
; Sequence 5, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-5

Query Match 40.4%; Score 201; DB 10; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 5 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 38

RESULT 9
US-10-077-438-1
; Sequence 1, Application US/10077438
; Patent No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Teschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech Rad S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-1

Query Match 40.4%; Score 201; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 34

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Db      8 CSQNEYPDSLHACIPCOLRCSSNTPPLTCORYC 41

RESULT 10
US-10-077-438-7
; Sequence 7, Application US/10077438
; Patent No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Teschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-7

Query Match      40.4%; Score 201; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCORYC 34
Db      8 CSQNEYPDSLHACIPCOLRCSSNTPPLTCORYC 41

RESULT 11
US-10-077-137-1
; Sequence 1, Application US/10077137
; Patent No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Teschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/283,447
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
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; ORGANISM: homo sapien
US-10-077-137-1

Query Match      40.4%; Score 201; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCORYC 34
Db      8 CSQNEYPDSLHACIPCOLRCSSNTPPLTCORYC 41

RESULT 12
US-10-077-137-7
; Sequence 7, Application US/10077137
; Patent No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Teschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-7

Query Match      40.4%; Score 201; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCORYC 34
Db      8 CSQNEYPDSLHACIPCOLRCSSNTPPLTCORYC 41

RESULT 13
US-10-068-725-2
; Sequence 2, Application US/10068725
; Publication No. US20030012783A1
; GENERAL INFORMATION:
; APPLICANT: Kindvogel, Wayne
; TITLE OF INVENTION: Antibodies That Bind Both BCMA and TACT
; FILE REFERENCE: 01-04
; CURRENT APPLICATION NUMBER: US/10/068,725
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/270,274
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/283,447
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-068-725-2

Query Match 40.4%; Score 201; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 34
DB 8 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 41

RESULT 14
US-09-854-864-12

; Sequence 12, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLVS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 117
; TYPE: PRT
; ORGANISM: human-murine Consensus
US-09-854-864-12

Query Match 30.7%; Score 153; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 CEYFDSLHACPCLRCSPTCQYC 58
DB 4 CEYFDSLHACPCLRCSPTCQYC 27

RESULT 15

US-09-854-864-10
; Sequence 10, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLVS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-854-864-10

Query Match 28.0%; Score 139.5; DB 10; Length 281;
Best Local Similarity 45.5%; Pred. No. 3.1e-05;
Matches 30; Conservative 3; Mismatches 16; Indels 17; Gaps 3;

QY 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYCEYFDSL-----HACPC 47

DB 5 CFHSEYFDSLHACPCHLRCSN--PPATCOPYCDPSVTSVKSGYTGCGGGGDKHTTCP- 61
QY 48 IRCSP 53
DB 62 -PCPAP 66

Search completed: February 4, 2003, 13:05:57
Job time : 6.24696 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 4, 2003, 12:52:56 ; Search time 20.6599 Seconds
(without alignments)
522.427 Million cell updates/sec

Title: us-09-854-864-13

Perfect score: 498
Sequence: 1 CSQNYRFDLLHACIPQLR.....SEYFDSLHACPPATCPYC 81

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

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23: /SIDP2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 205 | 41.2 | 302 | 22 | AAE00507 |
| 2 | 205 | 41.2 | 302 | 22 | AAE00507 |
| 3 | 201.5 | 40.5 | 283 | 22 | AAE06099 |
| 4 | 201 | 40.4 | 283 | 22 | AAE15488 |
| 5 | 201 | 40.4 | 34 | 23 | AAE15485 |
| 6 | 201 | 40.4 | 51 | 23 | AAE15485 |
| 7 | 201 | 40.4 | 58 | 23 | AAE15501 |
| 8 | 201 | 40.4 | 181 | 23 | AAE15484 |
| 9 | 201 | 40.4 | 184 | 21 | AAE08843 |
| 10 | 201 | 40.4 | 184 | 21 | AAE194001 |
| | | | 184 | 22 | AAE09241 |

| | | | | | | |
|----|-------|------|-----|----|----------|---------------------|
| 11 | 201 | 40.4 | 184 | 22 | AAE00506 | Human B cell matur |
| 12 | 201 | 40.4 | 184 | 22 | AAE06098 | Human BAF receptor |
| 13 | 201 | 40.4 | 184 | 22 | AAE19799 | Human B cell matur |
| 14 | 201 | 40.4 | 184 | 23 | AAE15487 | Human BCFM receptor |
| 15 | 159.5 | 32.0 | 157 | 22 | AAE07000 | Human BAF receptor |
| 16 | 153 | 30.7 | 224 | 23 | AAE15482 | Human-murine BCMA |
| 17 | 153 | 30.7 | 117 | 23 | AAE15491 | Human-murine B cell |
| 18 | 139.5 | 28.0 | 281 | 23 | AAE15489 | Mouse BCMA-human 1 |
| 19 | 136 | 27.3 | 185 | 21 | AAE08844 | Amino acid sequenc |
| 20 | 136 | 27.3 | 185 | 22 | AAE19800 | Murine B cell matur |
| 21 | 136 | 27.3 | 185 | 23 | AAE15480 | Mouse B cell matur |
| 22 | 100.5 | 20.2 | 334 | 23 | AAE14133 | Protein of hTACI (|
| 23 | 100.5 | 20.2 | 366 | 23 | AAE14132 | Protein of hTACI (|
| 24 | 98 | 19.7 | 249 | 21 | AAE19406 | A murine znf14, a |
| 25 | 96.5 | 19.4 | 301 | 22 | AAE19986 | Human protein SEQ |
| 26 | 95 | 19.1 | 256 | 22 | AAE08337 | Novel human diagno |
| 27 | 95 | 19.1 | 351 | 22 | AAE23698 | Novel human diagno |
| 28 | 93 | 18.7 | 166 | 19 | AAE15785 | Human lymphocyte s |
| 29 | 93 | 18.7 | 166 | 23 | AAE15494 | Human TACI splice |
| 30 | 93 | 18.7 | 265 | 22 | AAE09244 | Human TACI extrace |
| 31 | 93 | 18.7 | 291 | 23 | AAE10949 | Human AGP-3 recept |
| 32 | 93 | 18.7 | 293 | 19 | AAE15783 | Human lymphocyte s |
| 33 | 93 | 18.7 | 293 | 21 | AAE16312 | Human neutrophil-a |
| 34 | 93 | 18.7 | 293 | 21 | AAE19400 | A transmembrane ac |
| 35 | 93 | 18.7 | 293 | 22 | AAE09240 | Human TACI protein |
| 36 | 93 | 18.7 | 293 | 22 | AAE1914 | Human tumour necro |
| 37 | 93 | 18.7 | 293 | 23 | AAE19512 | Human TACI-IGF Fc |
| 38 | 93 | 18.7 | 293 | 23 | AAE1488 | Human TACI recepto |
| 39 | 93 | 18.7 | 293 | 23 | AAE14130 | Human transmembran |
| 40 | 93 | 18.7 | 293 | 23 | AAE15408 | Tumour necrosis fa |
| 41 | 93 | 18.7 | 293 | 23 | AAE15493 | Human transmembran |
| 42 | 93 | 18.7 | 293 | 23 | AAE09900 | Human AGP-3 relate |
| 43 | 93 | 18.7 | 312 | 23 | AAE14135 | Protein of N-termi |
| 44 | 93 | 18.7 | 397 | 23 | AAE15488 | Human TACI-immunog |
| 45 | 93 | 18.7 | 404 | 23 | AAE14136 | Protein of a compl |

ALIGNMENTS

| | | |
|----------|--|---|
| RESULT 1 | AAE00507 | standard; Protein; 302 AA. |
| ID | AAE00507 | |
| AC | AAE00507 | |
| XX | 31-JUL-2001 | (first entry) |
| DT | 31-JUL-2001 | (first entry) |
| XX | Human BCMA-Immunoglobulin G Fc region fusion construct. | |
| XX | Human: A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic; | |
| KW | gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease; | |
| KW | carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension; | |
| KW | systemic lupus erythematosus; SLE; inflammation; cardiovascular disease; | |
| KW | B-cell lympho-proliferative disorder; BCM; immunosuppressive disease; | |
| KW | organ transplantation; HIV; human immunodeficiency virus; TGF; murine; | |
| KW | tumour necrosis factor; B cell maturation protein; BCMA; fusion protein; | |
| KW | immunoglobulin G; IgG; Fc region. | |
| XX | | |
| OS | Chimeric - Homo sapiens. | |
| OS | Chimeric - Mus sp. | |
| XX | | |
| XX | Key | Location/Qualifiers |
| FT | Protein | 1..22 |
| FT | | /label= Signal_peptide |
| FT | | /note= "Derived from murine Ig kappa sequence" |
| FT | Protein | 23..302 |
| FT | | /label= Mature_human_BCMA_IgG_Fc_fusion_protein |
| FT | Region | 23..75 |
| FT | | /note= "Derived from human BCMA protein" |
| FT | Region | 76..302 |
| FT | | /note= "Derived from human IgG Fc region" |
| FT | Domain | 24..302 |

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FT      /label= Cysteine rich domain
PT      /note= "Derived From Human BCMA"
XX
XX      WO200124811-A1.
XX
XX      12-APR-2001.
XX
XX      05-OCT-2000; 2000WO-US27579.
XX
XX      06-OCT-1999; 99US-0157933.
XX      PR    11-FEB-2000; 2000US-0181807.
XX      PR    30-JUN-2000; 2000US-0215688.
XX
XX      (BIOJ ) BIOGEN INC.
XX      (AFOT-) APOTECH R & D SA.
XX
XX      Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;
XX      WPI: 2001-266242/27.
XX      N-PsDB; AAD03847.
XX
XX      Treating a mammal for a condition associated with undesired cell
XX      proliferation such as cancer or carcinoma, comprises administering a
XX      composition comprising A Proliferation Inducing Ligand Receptor
XX      (APRIIL-R) antagonist -
XX
XX      Example 1; Fig 3B; 85pp; English.
XX
XX      The invention relates to a method of treating a mammal for a condition
XX      associated with undesired cell proliferation such as cancer or
XX      carcinoma. The method involves administering a composition comprising
XX      A Proliferation Inducing Ligand Receptor (APRIIL-R) also referred as
XX      B cell maturation protein (BCM or BCMV) antagonist that antagonises the
XX      interaction between APRIIL and its cognate receptor(s). This method is
XX      useful for treating undesired cell proliferation such as cancer or
XX      carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
XX      prostate carcinoma, and other carcinomas whose proliferation is modulated
XX      by APRIIL. It is also useful for treating autoimmune diseases (Grave's
XX      disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular
XX      diseases, renal disorders, B-cell lympho-proliferative disorders,
XX      immunosuppressive diseases, organ transplantation, inflammation and
XX      human immunodeficiency virus (HIV), and for treating, suppressing or
XX      altering an immune response involving a signalling pathway between
XX      APRIIL-R and its ligand. APRIIL-R DNA is also useful in gene therapy.
XX      The present sequence is a fusion construct containing human APRIIL-R
XX      also referred as BCMV or BCM protein, Fc region of human immunoglobulin
XX      G (IgG) and a signal sequence from murine Ig kappa cDNA.
XX
XX      Sequence 302 AA;
XX
XX      Query Match          41.2%; Score 205; DB 22; Length 302;
XX      Best Local Similarity 67.8%; Pred. No. 2.3e-10;
XX      Matches 40; Conservative 2; Mismatches 9; Indels 8; Gaps 3
XX
Oy      1 CSQNEYFDSLHAACIPQCQRCSNTPPLTCQRYC-CERYDSTL-----LHACPCLRCSP 53
Db      31 CSQNEYPFDLSLHAACIPQCQRCSNTPPLTCQRCYNASVTNSVGVDKTHTCP--PCPAP 87
        ||| | | | | | | | | | | | | | | : | | | | | | | | | | | | | | |
ID      AAB60699 standard; Protein; 302 AA.
XX
XX      AAB60699;
XX
XX      22-MAY-2001 (first entry)
XX
XX      Mouse Igg signal/human BAFF-R/human Igg Fc fusion protein, BAFF-R-Fc.
XX
XX      Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
XX      immune-related disorder; B-cell growth inhibitor;
XX      B-cell maturation inhibitor; immunoglobulin production inhibitor;
XX      autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;

```

| | | |
|---|---|--|
| KM | | renal disorder; immunosuppressive disorder; HIV infection; |
| XK | | organ transplant; antiinflammatory; systemic lupus erythematosus; |
| KW | | autoimmune haemolytic anaemia; Grave's disease; multiple myeloma; |
| KV | | B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis; |
| KX | | Lymphoma; gene therapy; cancer; tumour; IgG Fc; fusion construct. |
| XX | | |
| OS | | Chimeric - Homo sapiens. |
| OS | | Chimeric - Mus sp. |
| PN | | WO200112812-A2. |
| PD | | 22-FEB-2001. |
| XX | | |
| PF | | 16-AUG-2000; 2000MO-US22507. |
| XX | | |
| PR | | 17-AUG-1999; 99US-0149378. |
| PR | | 11-FEB-2000; 2000US-0181684. |
| PR | | 18-FEB-2000; 2000US-0183536. |
| PA | (BIOJ) BIOGEN INC. | |
| XA | (APOT-) APOTECH R & D SA. | |
| XX | | |
| PI | Mackay F., Browning J., Ambrose C., Technop J., Schneider P; | |
| PI | Thompson J; | |
| DR | WIPI, 2001-202866/20. | |
| XX | N-PESDB; AAF59999. | |
| PT | Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell | |
| PT | lympho-proliferative disorder by administering BAFF-receptor | |
| PT | polypeptide, chimeric molecule comprising receptor or anti-BAFF-R | |
| PS | antibody homolog - | |
| Example 4; Fig 2; 59pp; English. | | |
| The invention relates to the use of a BAFF receptor (BAFF-R, also known as BCMA) protein, or a BAFF-R fusion protein as an agent for the treatment of a variety of immune-related disorders. BAFF-R is a member of the TNF (tumour necrosis factor) family, acting as an immunoregulatory agent, and also plays a role in the development of hypertension and related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-specific antibodies can be used for inhibiting B-cell growth, dendritic cell-induced B-cell growth and maturation, and immunoglobulin production, and in the treatment of autoimmune disorders, B-cell lymphoproliferative disorders, hypertension and renal disorders. The BAFF-R proteins may also be used in the treatment of immunosuppressive disorders and HIV infection, and in patients undergoing organ transplantation. The BAFF-R proteins or BAFF-R specific antibodies may be used for treating, suppressing or altering an immune response involving a signalling pathway between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R inhibits B-cell growth and maturation it is useful for treating diseases such as systemic lupus erythematosus, autoimmune haemolytic anaemia, Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly progressive glomerulonephritis, and lymphomas. Nucleic acids encoding human BAFF-R may be used in gene therapy to treat tumours, lymphomas, autoimmune disorders and inherited B-cell-associated disorders. The present sequence represents the BAFF-R fusion protein BAFF-R-Fc, comprising a mouse IgG-kappa signal sequence, residues 1-153 of human BAFF-R and a human IgG fc sequence. | | |
| SQ | Sequence 302 AA; | |
| Query Match | 41.2%; Score 205; DB 22; Length 302; | |
| Best Local Similarity | 67.8%; Pred. No. 2.3e-10; | |
| Matches 40; Conservative 2; Mismatches 9; Indels 8; Gaps 3 | | |
| Cy | 1 CSONEYPDSLHACIPCOLRGSSNTPLTCORYC-CSEYFDLSL-----LHACPCLRCSP 53 Db 31 CSQNYFPDSLHACTPCQLRCSSTNPPLTLCORYCAASVTNSVKGVDKHTCTCP--PCPPAP 87 | |
| RESULT 3 | | |
| AAE15488 | | |

| | |
|----|---|
| ID | AAE15488 standard; Protein; 283 AA. |
| XX | AAE15488; |
| XX | 12-MAR-2002 (first entry) |
| DE | Human BCMA-immunoglobulin Fc region fusion protein. |
| XX | Human; transmembrane activator and intracellular CAML interactor; TACI; cytosolic; B cell maturation protein; BCMa; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; proctitis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis; fusion protein. |
| KW | Homo sapiens. |
| OS | WO200187979-A2. |
| XX | 22-NOV-2001. |
| PD | 14-MAY-2001; 2001WD-US15567. |
| XX | 12-MAY-2000; 2000UB-204039P. |
| PR | 27-JUN-2000; 2000UB-214591P. |
| PR | 14-MAY-2001; 2001UB-0214591. |
| XX | (AMGE-) AMGEN INC. |
| PA | Theill LE, Yu G; |
| XK | WPI; 2002-066686/09. |
| DR | Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family ligand - |
| PT | Disclosure; Fig 10B; 94pp; English. |
| PS | The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMa) activity in a mammal. The method comprises administering a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF family ligand), having the consensus region of TACI, BCMa, or the TACI/BCMa extracellular consensus sequence, but not the extracellular region of TACI or BCMa. The method is useful for inhibiting activity of TACI and/or BCMa in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. APRIL, BCMa and TACI antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, proctitis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence is human BCMA protein-immunoglobulin Fc region fusion protein. |
| CC | Sequence 283 AA; |
| SQ | Query Match 40.5%; Score 201.5; DB 23; Length 283; Best Local Similarity 60.6%; Pred. No. 4,4e-10; Matches 40; Conservative 2; Mismatches 9; Indels 15; Gaps 3; |
| OY | 1 CSONEYFDSLTHAGCPCOLRGSSNTPPLTCQRYC-CYEYDLSL-----LHAGPC 47 DB 5 CSONEYFDSLTHAGCPCOLRGSSNTPPLTCQRYCNASVTNSVKGNAGGGGDKHTCP- 63 OY 48 LRCSP 53 |

| | | |
|---|---|---------------|
| DB | <div></div> | 64 - PCPAP 68 |
| RESULT 4 AAE15486 | | |
| ID | AAE15486 standard; peptide; 34 AA. | |
| XX | AAE15486; | |
| AC | | |
| XX | | |
| DT | 12-MAR-2002 (first entry) | |
| DE | Human B-cell maturation (BCMA) protein cysteine-rich consensus region. | |
| KW | Human; transmembrane activator and intracellular CAML interactor; TACT; cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis. | |
| KM | | |
| KX | | |
| PB | Homo sapiens. | |
| OS | | |
| PN | WO200187979-A2. | |
| PD | 22-NOV-2001. | |
| PR | 14-MAY-2001; 2001WO-US15567. | |
| PP | | |
| XX | 12-MAY-2000; 2000US-204039P. 27-JUN-2000; 2000US-214591P. 14-MAY-2001; 2001US-0214591. | |
| PA | (AMGE-) AMGEN INC. | |
| PI | Theill LE, Yu G; | |
| DR | WPI; 2002-066686/09. | |
| PT | Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family ligand | |
| PS | Claim 1; Fig 10A; 94pp; English. | |
| CC | The invention relates to a method for inhibiting TACT (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF family ligand), having the consenus sequence region of TACT, BCMA, or the TACT/ BCMA extracelllular consensus sequence, but not the extracelllular region of TACT or BCMA. The method is useful for inhibiting activity of TACT and/or BCMA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrintestinal, pancreatic or prostate tumour. APRIL, BCMA and TACT antagonists are useful for treating inflammation and immune function diseases such as diarrhea, psoriasis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence is human BCMA protein cysteine-rich consensus region. | |
| SO | Sequence 34 AA; | |
| Query Match 40.4%; Score 201; DB 23; Length 34; Best Local Similarity 100.0%; Pred. No. 7.Se-II; Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | |

OY 1 CSQNEYFDSLHACIPCQLRCSSTNPPLTCORYC 34

Db 1 CSQNEYFDSLHACIPCQLRCSSTNPPLTCORYC 34

RESULT 5
AAE15485

ID AAE15485 standard; peptide; 51 AA.

AC AAE15485;

DT 12-MAR-2002 (first entry)

DE Human B-cell maturation (BCMA) protein extracellular domain.

KM Human tumour necrosis factor receptor 1; TNF receptor 1
KM Cytotoxic T cell maturation protein; B2M; tumour necrosis factor; TNF
KM Lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic
KM prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KM drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KM Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KM human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KM rheumatoid arthritis; atherosclerosis.

OS Homo sapiens.

PN WO200187979-A2.

PD 22-NOV-2001

PF 14-MAY-2001; 2001WO-US15567

PR 12-MAY-2000; 2000US-204039P

PR 14-MAY-2001; 2001US-0214591

PA (AMGE-) AMGEN INC.

PI The11 LE, Yu G;

DR WPI, 2002-0666686/

PT Inhibiting activity

PT administering a binding partner for APRIL, a tumor necrosis factor

[illegible]

The invention relates to a method for inhibiting TAC1 (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for APRIL (670), a tumour necrosis factor- γ family ligand), having the consensus region of TAC1, BCMA, or the TAC1/BCMA extracellular consensus sequence, but not the extracellular region of TAC1 or BCMA. The method is useful for inhibiting activity of TAC1 and/or BCMA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TAC1 antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence is human BCMA protein extracellular domain.

SQ Sequence 51 AA;

Query Match 40.4%; Score 201; DB 23; Length 51;

Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0;
Gaps 0.

RESULT 6
AAE15501

ID AAE15501 standard; peptide; 58 AA.

AC AAE15501;

DT 12-MAR-2002 (first entry)

DE Human B cell maturation protein cysteine rich extracellular region

KM Human, transmembrane activator and intracellular CAML interactor; TAC1;
KM cytototoxic; B cell maturation protein; BCMA; tumour necrosis factor; TNF
KM lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic
KM prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KM drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KM Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KM human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KM rheumatoid arthritis; atherosclerosis.

OS Homo sapiens.

PN WO200187979-A2.

PD 22-NOV-2001

PF 14-MAY-2001; 2001WO-US15567.

PR 12-MAY-2000; 2000US-204039P.

PR 14-MAY-2001; 2001US-0214591.

PA (AMGE-) AMGEN INC.

PI Theill LE, Yu G;

DR WPI; 2002-066686/

PT Inhibiting activity

PT administering a binding partner for APRIL, a tumor necrosis factor

PS Disclosure; Fig 13; 94pp; English.

CC The invention relates to a method for inhibiting TAC1 (transmembrane
CC activator and intracellular CAM1 interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering
CC a specific binding partner for APRIL (G70, a tumour necrosis factor- α /TNF
CC family ligand), having the consensus region of TAC1, BCMA, or the TAC1/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TAC1 or BCMA. The method is useful for inhibiting activity of TAC1
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TAC1
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma), hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
CC is human BCMA cysteine-rich extracellular region.

SQ Sequence 58 AA;

Query Match 40.4%; Score 201; DB 23; Length 58;
 Best Local Similarity 100.0%; Pred. No. 1.2e-10;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34
 |||||
 Db 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34

RESULT 7

AAE15484
 ID AAE15484 standard; Protein; 181 AA.

AC AAE15484;

DT 12-MAR-2002 (first entry)

DE Human B-cell maturation (BCMA) protein.

KW Human; transmembrane activator and intracellular CAML interactor; TACI;
 KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis.

XX Homo sapiens.

XX Key Location/Qualifiers
 XX FH 5.38
 XX FT /note= "Cysteine-rich consensus region; This is region
 XX is specifically claimed as SEQ ID NO: 7 in claim 1 of
 XX the specification"

FT Domain 52..72
 FT /label= Transmembrane_domain

XX WO200187979-A2.

XX 22-NOV-2001.

XX 14-MAY-2001; 2001WO-US15567.

XX 12-MAY-2000; 2000US-204039P.

XX 27-JUN-2000; 2000US-214591P.

XX 14-MAY-2001; 2001US-0214591.

XX (AMGE-) AMGEN INC.

XX The111 LE, Yu G;

XX WPI; 2002-066686/09.

PT Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor
 PT family ligand -

XX Disclosure; Fig 10A; 94pp; English.

XX The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering
 CC a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region, of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function

CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human BCMA protein.

XX Sequence 181 AA;

Query Match 40.4%; Score 201; DB 23; Length 181;
 Best Local Similarity 100.0%; Pred. No. 3.3e-10;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34
 |||||
 Db 5 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 38

RESULT 8

AAE08843
 ID AAE08843 standard; peptide; 184 AA.

AC AAE08843;

DT 02-JAN-2001 (first entry)

DE Amino acid sequence of human.

XX BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer;
 KW anti-cell death gene; apoptosis; viral infection; inflammatory response;
 KW rheumatoid arthritis; inflammatory bowel disease; septic shock.

XX Homo sapiens.

XX Key Location/Qualifiers
 XX FH 57..77
 XX FT Domain /note= "putative transmembrane domain"

XX WO200050633-A1.

XX 31-AUG-2000.

XX 24-FEB-2000; 2000WO-US04925.

XX 24-FEB-1999; 99US-0121485.

XX (GENO) GEN HOSPITAL CORP.

XX Seed B, Ting A;

XX WPI; 2000-558405/51.

PT Identifying a modulator of gene expression for drug designing, by
 PT contacting a compound library with a cell expressing an anti-cell death
 PT gene and reporter gene, and determining alteration in reporter gene
 PT expression -

XX Claim 32; Fig 7A; 53pp; English.

XX The present sequence represents a BCMA (not defined) polypeptide. BCMA
 CC is a necrosis factor (NF)-kB activator. The method of the invention is
 CC used to identify compounds which modulate BCMA activity (and thus NF-kB
 CC activity). The specification describes a method of identifying a
 CC polypeptide which increases gene expression from a promoter. The method
 CC involves contacting a library of with a cell which expresses a
 CC recombinant anti-cell death gene and a reporter gene operably linked to
 CC the promoter, and then determining whether the expression of the
 CC reporter gene is altered as a result of contact with library. The method
 CC is useful for identifying polypeptides which increase or decrease gene
 CC expression from a promoter. The BCMA polypeptide or nucleic acid are
 CC useful for preparing a pharmaceutical composition for treating cancer,

CC apoptosis, viral infections, inflammatory response, such as rheumatoid
CC arthritis, inflammatory bowel disease or septic shock. BCMA is useful for
CC identifying compounds that modulate NF-kB expression and thus for drug
CC designing.

SO Sequence 184 AA;

Query Match 40.4%; Score 201; DB 21; Length 184;
Best Local Similarity 100.0%; Pred. No. 3,4e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSONEYFDSLHACIPCOLRGSSNTPPLTCORYC 34
Db 8 GSONEYFDSLHACIPCOLRGSSNTPPLTCORYC 41

RESULT 9
AA94001
ID AA94001 standard; Protein; 184 AA.

AC AA94001;
DT 20-OCT-2000 (first entry)

XX A human BCMA protein, a B cell protein related to TACI.

XX Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
KM transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
KM ztnf4 activity; antibody production; autoimmune disease; amyloidosis;
KM systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
KM rheumatoid arthritis; aetna; bronchitis; emphysema; pyelonephritis;
KM end stage renal failure; glomerulonephritis; vasculitis; nephritis;
KM renal neoplasia; multiple myeloma; lymphoma; light chain neuropathy;
KM immune response; immunosuppression; graft rejection; joint pain;
KM graft versus host disease; inflammation; swelling; anaemia; septic shock;
KM insulin dependent diabetes mellitus; Crohn's disease; hypertension;
KM renal artery stenosis; occlusion; cholesterol; renal emboli.

XX Homo sapiens.

OS WO20040716-A2.

PN 13-JUL-2000.

XX 07-JAN-2000; 2000WO-US00396.

PR 07-JAN-1999; 99US-0226533.

XX (ZYMO) ZYMOGENETICS INC.

PA Gross JA, Xu W, Madden K, Yee DP;

PI MPI; 2000-452538/39.

DR N-PSDB; AAS58559.

XX Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,
PT renal disease, graft versus host disease, and inflammation, comprises
PT administering a BR43x2, TACI or BCMA extracellular domain polypeptide -

XX Disclosure; Page 152, 175pp; English.

XX The present sequence represents a human BCMA protein, a B cell protein
CC related to transmembrane activator and CAML-interactor (TACI) receptor.
CC TACI is a tumour necrosis factor (TNF) receptor. The extracellular
CC domain of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell
CC protein) receptor contain a cysteine rich domain, and are used for
CC inhibiting ztnf4 activity. Ztnf4 is a TNF ligand. They may also be used
CC for inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated
CC with activated or resting B lymphocytes, effector T-cells, or with
CC antibody production. The antibody production is associated with an
CC autoimmune disease selected from systemic lupus erythematosus, myasthenia
CC gravis, multiple sclerosis and rheumatoid arthritis. The ztnf4 activity
CC and BR43x2, TACI or BCMA receptor-ligand engagement is associated with

CC asthma, bronchitis, emphysema, end stage renal failure,
CC glomerulonephritis, vasculitis, nephritis, pyelonephritis, renal
CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy,
CC amyloidosis, moderating immune response, immunosuppression, graft
CC rejection, graft versus host disease, inflammation, insulin dependent
CC diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or
CC septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies,
CC agonists or antagonists can be used to treat hypertension, renal artery
CC stenosis, or occlusion, and cholesterol or renal emboli.

SO Sequence 184 AA;

Query Match 40.4%; Score 201; DB 21; Length 184;
Best Local Similarity 100.0%; Pred. No. 3,4e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSONEYFDSLHACIPCOLRGSSNTPPLTCORYC 34
Db 8 GSONEYFDSLHACIPCOLRGSSNTPPLTCORYC 41

RESULT 10
AAE09241
ID AAE09241 standard; Protein; 184 AA.

XX AAE09241;

DT 19-NOV-2001 (first entry)

XX Human BCMA protein.

XX Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor;
KM TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
KM autoimmune disease; rheumatoid arthritis; multiple sclerosis;
KM psoriasis.

XX Homo sapiens.

OS WO200160397-A1.

PN 23-AUG-2001.

XX 28-NOV-2000; 2000WO-US32378.

PR 16-FEB-2000; 2000US-0182938.

XX 22-AUG-2000; 2000US-0226986.

XX (GETH) GENENTECH INC.

PA Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pletti RM;

PI Yan M;

DR MPI; 2001-541628/60.

XX Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
PT activity, for treating autoimmune disorders and cancer, comprises
PT exposing the cells to TALL-1 or APRIL polypeptide agonists or
PT antagonists -

XX Example 2; Fig 2; 160pp; English.

XX The invention relates to methods of using one or more agonists or
CC antagonists to modulate the activity of the members of TNF (tumour
CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR)
CC e.g. TACI or BCMA. The method is useful for treating pathological
CC conditions or diseases associated with increased TALL-1 and APRIL
CC expression or activity. TALL-1 and APRIL antagonists are used to
CC block the interaction between APRIL and TALL-1 with TACI or BCMA.
CC They are useful for treating a mammal suffering from cancer such
CC as leukaemia, lymphoma, myeloma, cancers of lung and colon and
CC autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis,
CC psoriasis and lupus erythematosus. The present sequence is human

CC BCMA protein.
 XX Sequence 184 AA;
 SQ Query Match 40.4%; Score 201; DB 22; Length 184;
 Beat Local Similarity 100.0%; Pred. No. 3.4e-10;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CSQNEYPDSLHACIPCOLRCSSTNPPLTCQRYC 34
 DB 8 CSQNEYPDSLHACIPCOLRCSSTNPPLTCQRYC 41

RESULT 11
 ID AAE00506 standard; Protein; 184 AA.
 XX AAE00506;
 AC AAE00506;
 DT 31-JUN-2001 (first entry)
 XX Human B cell maturation protein (BCMA).
 DE Human, A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;
 KM gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;
 KM carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;
 KM systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
 KM B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;
 KM organ transplantion; HIV; human immunodeficiency virus; TNF;
 KM tumour necrosis factor; BCMA; B cell maturation protein.
 KM Homo sapiens.
 OS Homo sapiens.
 XX WO200124811-A1.
 PN 12-APR-2001.
 XX 05-OCT-2000; 2000WD-US27579.
 XX 06-OCT-1999; 99US-0157933.
 PR 11-FEB-2000; 2000US-0181807.
 PR 30-JUN-2000; 2000US-0215688.
 XX (BIOJ) BIOGEN INC.
 PA (APOT-) APOTEC R & D SA.
 XX Schneider P, Thompson J, Cachero T, Ambrose C, Rennett P;
 PI WPI, 2001-266242/27.
 DR N-PSDB; AAD03844.
 XX Treating a mammal for a condition associated with undesired cell
 PT proliferation such as cancer or carcinoma, comprises administering a
 FT composition comprising A Proliferation Inducing Ligand Receptor
 PT (APRIL-R) antagonist.
 PS Claim 3; Fig 3A; 85pp; English.
 XX The invention relates to a method of treating a mammal for a condition
 CC associated with undesired cell proliferation such as cancer or
 CC carcinoma. The method involves administering a composition comprising
 CC A Proliferation Inducing Ligand Receptor (APRIL-R) also referred as
 CC B cell maturation protein (BCM or BCMA) antagonist that antagonises the
 CC interaction between APRIL and its cognate receptor(s). This method is
 CC useful for treating undesired cell proliferation such as cancer or
 CC carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
 CC prostate carcinoma, and other carcinomas whose proliferation is modulated
 CC by APRIL. It is also useful for treating autoimmune diseases (Grave's
 CC disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular
 CC diseases, renal disorders, B-cell lympho-proliferative disorders,
 CC immunosuppressive diseases, organ transplantion, inflammation and
 CC human immunodeficiency virus (HIV), and for treating, suppressing or
 CC altering an immune response involving a signalling pathway between

CC APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy.
 CC The present sequence is human APRIL-R also referred as BCMA or
 CC BCM protein.
 XX Sequence 184 AA;
 SQ Query Match 40.4%; Score 201; DB 22; Length 184;
 Beat Local Similarity 100.0%; Pred. No. 3.4e-10;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CSQNEYPDSLHACIPCOLRCSSTNPPLTCQRYC 34
 DB 8 CSQNEYPDSLHACIPCOLRCSSTNPPLTCQRYC 41

RESULT 12
 ID AAB60698 standard; Protein; 184 AA.
 XX AAB60698;
 AC AAB60698;
 DT 22-MAY-2001 (first entry)
 XX Human BAFF receptor (BAFF-R).
 DE Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
 XX immune-related disorder; B-cell growth inhibitor; BCMA;
 KM B-cell maturation inhibitor; immunoglobulin production inhibitor;
 KM autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
 KM renal disorder; immunosuppressive disorder; HIV infection;
 KM organ transplantion; antiinflammatory; systemic lupus erythematosus;
 KM autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
 KM B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
 KM lymphoma; gene therapy; cancer; tumour.
 KM Homo sapiens.
 OS Homo sapiens.
 XX WO200112812-A2.
 PN 22-FEB-2001.
 XX 16-AUG-2000; 2000WO-US22507.
 XX 17-AUG-1999; 99US-0149378.
 PR 11-FEB-2000; 2000US-0181684.
 PR 18-FEB-2000; 2000US-0183536.
 XX (BIOJ) BIOGEN INC.
 PA (APOT-) APOTEC R & D SA.
 XX Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;
 PI Thompson J;
 DR WPI, 2001-202866/20.
 DR N-PSDB; AAF59998.
 XX Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
 PT lympho-proliferative disorder by administering BAFF-receptor
 FT polypeptide, chimeric molecule comprising receptor or anti-BAFF-R
 PT antibody homolog.
 PS Claim 20; Fig 1; 59pp; English.
 XX The invention relates to the use of a BAFF receptor (BAFF-R, also known
 CC as BCMA) protein, or a BAFF-R fusion protein as an agent for the
 CC treatment of a variety of immune-related disorders. BAFF-R is a member of
 CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory
 CC agent, and also plays a role in the development of hypertension and
 CC related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-
 CC specific antibodies can be used for inhibiting B-cell growth, dendritic
 CC cell-induced B-cell growth and maturation, and immunoglobulin production,
 CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative
 CC disorders, hypertension and renal disorders. The BAFF-R proteins may also

CC be used in the treatment of immunosuppressive disorders and HIV
 CC infection, and in patients undergoing organ transplantation. The BAPF-R
 CC protein or BAPF-R specific antibodies may be used for treating,
 CC suppressing or altering an immune response involving a signalling pathway
 CC between BAPF-R and BAPF, thereby inhibiting inflammation. Since BAPF-R
 CC inhibits B-cell growth and maturation it is useful for treating diseases
 CC such as systemic lupus erythematosus, autoimmune hemolytic anaemia,
 CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
 CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
 CC human BAPF-R may be used in gene therapy to treat tumours, lymphomas,
 CC autoimmune disorders and inherited B-cell-associated disorders. The
 CC present sequence represents human BAPF-R.

XX Sequence 184 AA;

Query Match 40.4%; Score 201; DB 22; Length 184;
 Best Local Similarity 100.0%; Pred. No. 3.4e-10;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRGSSNTPPLTCORYC 34
 |||
 DB 8 CSQNEYFDSLHACIPCOLRGSSNTPPLTCORYC 41

RESULT 13
 AAY71979
 ID AAY71979 standard; Protein; 184 AA.

AC AAY71979;
 XX
 DT 28-MAR-2001 (first entry)

DE Human B cell maturation factor (BCMA) protein.

XX
 KW Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
 KW Tumour necrosis factor and Apol-related leucocyte expressed ligand 1;
 KW therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
 KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
 KW thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;
 KW haemolytic anaemia; Grave's disease; myasthenia gravis; chromosome 16;
 KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;
 KW B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.

OS Homo sapiens.

XX
 FH Key Location/Qualifiers
 FT Domain 1..62
 FT /label= Extracellular_domain

XX WO20068378-A1.

XX 16-NOV-2000.

XX 05-MAY-2000; 2000WO-US12266.

XX 06-MAY-1999; 99US-0132892.

XX 01-MAY-2000; 2000US-0201012.

XX (NAJE-) NAT JEWISH MEDICAL & RES CENT.

XX Shu HS;

XX WPI, 2001-016094/02.

XX N-PSDB; AAD02125.

XX Isolated TALL-1 protein is used to identify compounds that regulate B
 XX lymphocyte proliferation, used to treat B lymphocyte associated
 XX autoimmune disorders -

XX Claim 37; Page 104-105; 112pp; English.

XX The present invention relates to Tumour necrosis factor (TNF) and
 CC Apol-related leucocyte expressed ligand 1 (TALL-1) nucleic acid

CC molecules, proteins (including homologues), and their antibodies. The
 CC invention in particular relates to methods for regulating the
 CC interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell
 CC maturation factor) to regulate monocyte, macrophage and B lymphocyte
 CC mediated immune responses. TALL-1 protein is useful for identifying
 CC compounds that regulate B lymphocyte proliferation. It is also useful for
 CC treating B lymphocyte associated autoimmune disorders like rheumatoid
 CC arthritis, systemic lupus erythematosus (SLE), insulin dependent diabetes
 CC mellitus, multiple sclerosis, myasthenia gravis, Grave's disease,
 CC autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura,
 CC Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever,
 CC post-streptococcal glomerulonephritis or polyarteritis nodosa.
 CC The TALL-1 protein and its corresponding nucleic acid sequence are also
 CC useful in diagnostic assays.
 CC The present sequence is a human B cell maturation factor (BCMA)
 CC protein. It is the receptor for TALL-1 protein. BCMA gene is
 CC located on chromosome 16. In human tissues, BCMA is expressed by
 CC spleen and lymph nodes but not by brain, muscle, heart, lung, kidney,
 CC pancreas, testis and placenta. BCMA mRNA is absent in the pro-B
 CC lymphocyte stage but its expression increases with B lymphocyte
 CC maturation.

XX Sequence 184 AA;

Query Match 40.4%; Score 201; DB 22; Length 184;
 Best Local Similarity 100.0%; Pred. No. 3.4e-10;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRGSSNTPPLTCORYC 34
 |||
 DB 8 CSQNEYFDSLHACIPCOLRGSSNTPPLTCORYC 41

RESULT 14
 ABB81487
 ID ABB81487 standard; Protein; 184 AA.

XX ABB81487;

XX 02-SEP-2002 (first entry)

DE Human BCMA receptor related protein SEQ ID NO:7.

XX
 KW Human; Znfir12; tumour necrosis factor receptor; cytosolic;
 KW immunosuppressive; dermatological; antiinflammatory; antidiabetic;
 KW neuroprotective; antirheumatic; antiallergic; antiaesthetic;
 KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
 KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
 KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;
 KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
 KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
 KW pyleonephritis; renal neoplasia; multiple myeloma; amyloidosis;
 KW light chain neuropathy; hypertension; large vessel disease;
 KW graft-versus host disease; graft rejection; Crohn's disease.

XX Homo sapiens.

XX WO200238766-A2.

XX 16-MAY-2002.

XX 05-NOV-2001; 2001WO-US47018.

XX 07-NOV-2000; 2000US-24649P.

XX 20-DEC-2000; 2000US-257131P.

XX 28-JUN-2001; 2001US-301715P.

XX 29-AUG-2001; 2001US-315565P.

XX (ZYMO) ZYMOGENETICS INC.

XX Gross JA, Xu W, Heme RM, Grant FU;

XX WPI, 2002-508212/54.

XX Novel isolated human tumor necrosis factor receptor polypeptide, termed
 PT Znfir12, useful for treating autoimmune disorders, emphysema, end
 PT stage renal failure or renal disease and lymphoma
 XX
 PS Disclosure; Page 135-136; 154pp; English.

XX The present invention describes a human tumour necrosis factor receptor
 CC designated Znfir12 (I). (I) has cytostatic, immunosuppressive,
 CC dermatological, antiinflammatory, neuroprotective, antidiabetic,
 CC antineumatic, antirheumatic, antiashtmatic, nephrotropic and hypotensive
 CC activities, and can be used in gene therapy. (I) can be used for
 CC inhibiting, in a mammal, the activity of a ligand that binds Znfir12
 CC (e.g. ZTNF4), for treating disorders and diseases associated with B
 CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
 CC inhibiting the proliferation of tumour cells. (I) is useful for treating
 CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
 CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
 CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
 CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
 CC leukaemia, nephritis, and pyelonephritis, and for treating renal
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
 CC amyloidosis, hypertension, large vessel diseases, graft-versus host
 CC disease, graft rejection and Crohn's disease. (I) is useful for
 CC modulating the immune system, for regulating B cell responses and
 CC development, for modulating development of other cells, antibody
 CC production and cytokine production, and for modulating T and B cell
 CC communication. The present sequence represents a protein which is
 CC given in the exemplification of the present invention.

XX Sequence 184 AA;
 SQ

Query Match 40.4%; Score 201; DB 23; Length 184;
 Best Local Similarity 100.0%; Pred. No. 3,4e-10;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSQNEFYPSLHACIPQCRSSNTPPLTCQRYC 34
 Db 8 CSQNEFYPSLHACIPQCRSSNTPPLTCQRYC 41

RESULT 15
 AAB60700 ID AAB60700 standard; Protein; 157 AA.
 XX AC AAB60700;
 XX 22-MAY-2001 (first entry)
 XX Human BAPF receptor (BAPF-R) sequence encoded by A plasmid pJST535.
 XX
 KW Human BAPF-R; BAPF receptor; TNF family; immunoregulatory agent;
 KW immune-related disorder; B-cell growth inhibitor; BCMA; inhibitor;
 KW B-cell maturation inhibitor; immunoglobulin production inhibitor;
 KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
 KW renal disorder; immunosuppressive disorder; HIV infection;
 KW organ transplantation; antiinflammatory; systemic lupus erythematosus;
 KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
 KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
 KW lymphoma; gene therapy; cancer; tumour; plasmid pJST535.
 XX
 XX Homo sapiens.
 OS
 PN WO200112812-A2.
 PD 22-FEB-2001.
 XX
 PF 16-AUG-2000; 2000WD-US22507.
 XX
 PR 17-AUG-1999; 99US-0149378.
 PR 11-FEB-2000; 2000US-0181684.
 PR 18-FEB-2000; 2000US-0183536.
 XX

PA (BIOJ) BIOGEN INC.
 PA (APOT-) APOTEC R & D SA.
 XX
 XX Mackay F, Browning J, Ambrose C, Teichopp J, Schneider P;
 PI Thompson J;
 XX
 XX WPI; 2001-202866/20.
 DR N-PSDB; AAF60000.
 XX
 XX Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
 PT lymphoproliferative disorder by administering BAPF-receptor
 PT polypeptide, chimeric molecule comprising receptor or anti-BAPF-R
 PT antibody homolog -
 XX
 XX Example 1; Fig 3; 59pp; English.

XX The invention relates to the use of a BAPF receptor (BAPF-R, also known
 CC as BCMA) protein, or a BAPF-R fusion protein as an agent for the
 CC treatment of a variety of immune-related disorders. BAPF-R is a member of
 CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory
 CC agent, and also plays a role in the development of hypertension and
 CC related disorders. BAPF-R, fusion proteins containing it, and BAPF-R-
 CC specific antibodies can be used for inhibiting B-cell growth, dendritic
 CC cell-induced B-cell growth and maturation, and immunoglobulin production,
 CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative
 CC disorders, hypertension and renal disorders. The BAPF-R proteins may also
 CC be used in the treatment of immunosuppressive disorders and HIV
 CC infection, and in patients undergoing organ transplantation. The BAPF-R
 CC proteins or BAPF-R specific antibodies may be used for treating,
 CC suppressing or altering an immune response involving a signalling pathway
 CC between BAPF-R and BAPF, thereby inhibiting inflammation. Since BAPF-R
 CC inhibits B-cell growth and maturation it is useful for treating diseases
 CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
 CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
 CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
 CC human BAPF-R may be used in gene therapy to treat tumours, lymphomas,
 CC autoimmune disorders and inherited B-cell-associated disorders. The
 CC present sequence represents a human BAPF-R protein sequence as encoded
 CC by plasmid pJST535. However, this BAPF-R protein sequence is 27 amino
 CC acids shorter than that given in AAB60698.

XX Sequence 157 AA;
 SQ

Query Match 32.0%; Score 159.5; DB 22; Length 157;
 Best Local Similarity 90.6%; Pred. No. 1,1e-06;
 Matches 29; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

OY 3 QNEFYPSLHACIPQCRSSNTPPLTCQRYC 34
 Db 7 QNEFYPSLHACIPQCRSSNTPPLTCQRYC 35

Search completed: February 4, 2003, 12:57:44
 Job time : 21.6599 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: February 4, 2003, 12:53:41 / Search time 17.3806 Seconds
(without alignments)
960.257 Million cell updates/sec

Title: US-09-854-864-13

Perfect score: 498

Sequence: 1 CSQNEVFDSLHACIPQCLR.....SEYFDSLHACPPATCPYC 81

Scoring table: BLOSUM62

Searched: Gapop 10.0, Gapext 0.5

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Listing first 45 summaries

SPREMBL_21:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_phc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_prodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 100.5 | 20.2 | 1792 | 13 | 057484 gallus gall |
| 2 | 94.5 | 19.0 | 223 | 11 | 062220 mus musculu |
| 3 | 94.5 | 19.0 | 230 | 11 | 064507 mus musculu |
| 4 | 93.5 | 18.8 | 195 | 11 | 09D141 mus musculu |
| 5 | 92.5 | 18.6 | 169 | 4 | 014564 mus musculu |
| 6 | 92.5 | 18.6 | 227 | 11 | 09D225 mus musculu |
| 7 | 91.5 | 18.4 | 136 | 4 | 09BYR2 mus sapien |
| 8 | 91.5 | 18.4 | 186 | 4 | 09BYR2 mus sapien |
| 9 | 91.5 | 18.4 | 186 | 11 | 064526 mus musculu |
| 10 | 91.5 | 18.4 | 191 | 11 | 09D3H7 mus sapien |
| 11 | 89 | 17.9 | 159 | 4 | 09BYQ3 mus sapien |
| 12 | 89 | 17.9 | 1574 | 11 | 088281 rattus norv |
| 13 | 88 | 17.7 | 166 | 4 | 09BYR3 mus sapien |
| 14 | 87.5 | 17.6 | 154 | 4 | 09BYQ2 mus sapien |
| 15 | 87.5 | 17.6 | 174 | 4 | 09BYQ4 mus sapien |
| 16 | 87.5 | 17.6 | 193 | 4 | 09BYQ5 mus sapien |

| | | | | | |
|----|------|------|------|----|--------------------|
| 17 | 87 | 17.5 | 159 | 4 | 09BYQ0 mus sapien |
| 18 | 87 | 17.5 | 165 | 11 | 09D7P3 mus musculu |
| 19 | 87 | 17.5 | 195 | 11 | 09D0X9 mus musculu |
| 20 | 87 | 17.5 | 1376 | 5 | 08SZS2 drosophila |
| 21 | 87 | 17.5 | 1679 | 5 | 024301 drosophila |
| 22 | 86 | 17.3 | 188 | 11 | 070148 rattus norv |
| 23 | 86 | 17.3 | 2112 | 5 | 08WPL0 mus sapien |
| 24 | 85.5 | 17.2 | 154 | 4 | 09BYP9 mus sapien |
| 25 | 85.5 | 17.2 | 177 | 11 | 09D644 mus musculu |
| 26 | 85.5 | 17.2 | 189 | 11 | 09D527 mus musculu |
| 27 | 85 | 17.1 | 202 | 11 | 091W93 mus musculu |
| 28 | 85 | 17.1 | 325 | 10 | 094HS1 oryza sativ |
| 29 | 84.5 | 17.0 | 767 | 13 | 09DGR2 xenopus lae |
| 30 | 84 | 16.9 | 195 | 4 | 09BYQ6 mus sapien |
| 31 | 84 | 16.9 | 201 | 4 | 09BQ06 mus sapien |
| 32 | 84 | 16.9 | 210 | 4 | 09BYR0 mus sapien |
| 33 | 84 | 16.9 | 1671 | 5 | 09NJV5 biophalari |
| 34 | 83.5 | 16.8 | 110 | 5 | 09BIR2 paramecium |
| 35 | 83.5 | 16.8 | 130 | 11 | 09Z287 mus musculu |
| 36 | 83.5 | 16.8 | 191 | 4 | 09BYQ8 mus sapien |
| 37 | 83 | 16.7 | 175 | 4 | 007628 mus sapien |
| 38 | 82 | 16.5 | 98 | 4 | 09BYR8 mus sapien |
| 39 | 82 | 16.5 | 126 | 6 | 028707 oryctolagus |
| 40 | 82 | 16.5 | 167 | 11 | 09D122 mus musculu |
| 41 | 82 | 16.5 | 168 | 11 | 09D732 mus musculu |
| 42 | 81.5 | 16.4 | 85 | 11 | 070555 mus musculu |
| 43 | 81.5 | 16.4 | 429 | 13 | 091650 xenopus lae |
| 44 | 81 | 16.3 | 353 | 5 | 09VW81 drosophila |
| 45 | 81 | 16.3 | 353 | 5 | 08SZS8 drosophila |

ALIGNMENTS

RESULT 1

ID 057484 PRELIMINARY; PRT; 1792 AA.

AC 057484; 01-JUN-1998 (TREMBLERel. 06, Created)

DT 01-JUN-1998 (TREMBLERel. 06, Last sequence update)

DT 01-JUN-2002 (TREMBLERel. 21, Last annotation update)

DE Laminin beta 2-like chain.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; OC Gallus.

CX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93015947; PubMed=1400373;

RA O'Rear J.J.;

RT "A novel laminin B1 chain variant in avian eye.";

RL J. Biol. Chem. 267:20555-20557 (1992).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=98209634; PubMed=9550264;

RA Liu J., Swadlow S., Xie W., Brewton R.G., Mayne R.;

RT evidence for four beta chains in birds.";

RL Matrix Biol. 16:471-481 (1998).

DR EMBL; AF038555; AAB92586.1; -.

DR HSSP; P02468; IKLO.

DR InterPro; IPR002106; AATRNA_ligaseII.

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR002049; Laminin_EGF.

DR InterPro; IPR001866; Laminin.

DR Pfam; PF00053; laminin_EGF_13.

DR Pfam; PF00053; laminin_Nterm_1.

DR PRINTS; PR00011; EGFATMININ.

DR SMART; SMO0180; EGF_Iam; 13.

DR SMART; SMO0136; LaminT; 1.

DR PROSITE; PS00339; AA_TENA_LIGASE_II_2; UNKNOWN_1.

DR PROSITE; PS00022; EGF_1; UNKNOWN_10.

DR PROSITE; PS01186; EGF 2; 2.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; 12. EGF-like domain, Repeat.
 KM EGF-like domain; Glycoprotein; Laminin domain.
 SQ SEQUENCE 1792 AA; 195723 MW; 4A4CB80206FA600 CRC64;

Query Match 20.2%; Score 100.5; DB 13; Length 1792;
 Best Local Similarity 32.0%; Pred. No. 0.00059;
 Matches 32; Conservative 8; Mismatches 35; Indels 25; Gaps 6;

QY 1 CSQNEFYDSLHACIPQCRSSNTPPLTCQRYCCCEFYDSLHACPCRCSPPTQYCCF 49
 DB 1017 CQPGYGDAMRHS---RRCSCNTLTGTBPNTCGPQCCQDQSGGCHCLPHVEGSCDR 1072
 QY 50 CSP-----PTQYCCCHSEFYDSLHACPCATQPYC 81
 DB 1073 CSPNFMNLGSGGCEPCACHPQH--SLSPACNQPTGQSCC 1110

RESULT 2

Q62220 PRELIMINARY; PRT; 223 AA.
 AC Q62220;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Serine 2 ultra high sulfur protein.
 GN KRTAP5-4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxId=10090;
 RN NCB1 (1)
 RC STRAIN=BALB/C;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91065960; PubMed=2250030;
 RA Wood L., Mills M., Hatzenbuehler N., Vogel G.;
 RT "Serine-rich ultra high sulfur protein gene expression in murine hair
 RT and skin during the hair cycle.";
 RL J. Biol. Chem. 265:21375-21380(1990).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RX MEDLINE=91154184; PubMed=1840598;
 RA Wood L., Mills M., Hatzenbuehler N., Vogel G.;
 RT "Additions and Corrections: Serine-rich ultra high sulfur protein gene
 RT expression in murine hair and skin during the hair cycle.";
 RL J. Biol. Chem. 266:4024-4024(1991).
 DR EMBL; M37760; AAA40107.1; -.
 DR HSRF; P01064; IPT2.
 DR MGD; MGI:1354758; Krtap5-4.
 DR InterPro; IPR001450; 4Fe4S_ferredoxin.
 DR InterPro; IPR001007; VWF_C.
 DR PROSITE; PS00198; 4Fe4S_FERREDOXIN; UNKNOWN_2.
 DR PROSITE; PS01208; VWF_C; UNKNOWN_2.
 SQ SEQUENCE 223 AA; 21442 MW; C654BDB9FD08C59A CRC64;

Query Match 19.0%; Score 94.5; DB 11; Length 223;
 Best Local Similarity 29.6%; Pred. No. 0.00052;
 Matches 24; Conservative 3; Mismatches 27; Indels 27; Gaps 5;

QY 1 CSQNEFYDSLHACIPQCRSSNTPPLTCQRYCCCEFYDSLHACPCRCSPPTQYCCF 60
 DB 150 CQSS-----CCKPC-----CSCGSSCCGSSCC-----PCC-CGSSCCCKPCC 189
 QY 61 HSEYFDSLHACPCATQPYC 81
 DB 190 QSS-----CCKPCCCGSSC 203

RESULT 3
 Q64507 PRELIMINARY; PRT; 230 AA.
 AC Q64507;

DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Serine 1 ultra high sulfur protein.
 GN KRTAP5-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxId=10090;
 RN NCB1 (1)
 RC STRAIN=BALB/C;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91065960; PubMed=2250030;
 RA Wood L., Mills M., Hatzenbuehler N., Vogel G.;
 RT "Serine-rich ultra high sulfur protein gene expression in murine hair
 RT and skin during the hair cycle.";
 RL J. Biol. Chem. 265:21375-21380(1990).
 DR EMBL; M37759; AAA40106.1; -.
 DR HSRF; P01064; IPT2.
 DR MGD; MGI:1354732; Krtap5-1.
 DR InterPro; IPR001450; 4Fe4S_ferredoxin.
 DR InterPro; IPR000020; Anaphylatoxin.
 DR InterPro; IPR001305; DnaJ_CXXCXXG.
 DR InterPro; IPR001007; VWF_C.
 DR PROSITE; PS00198; 4Fe4S_FERREDOXIN; UNKNOWN_1.
 DR PROSITE; PS01177; ANAPHYLATOXIN_1; UNKNOWN_1.
 DR PROSITE; PS00637; DnaJ_CXXCXXG; UNKNOWN_1.
 DR PROSITE; PS01208; VWF_C; UNKNOWN_3.
 SQ SEQUENCE 230 AA; 21781 MW; FCC50B41B2137C23 CRC64;

Query Match 19.0%; Score 94.5; DB 11; Length 230;
 Best Local Similarity 29.6%; Pred. No. 0.00053;
 Matches 24; Conservative 3; Mismatches 27; Indels 27; Gaps 5;

QY 1 CSQNEFYDSLHACIPQCRSSNTPPLTCQRYCCCEFYDSLHACPCRCSPPTQYCCF 60
 DB 149 CQSS-----CCKPC-----CSCGSSCCGSSCC-----PCC-CGSSCCCKPCC 188
 QY 61 HSEYFDSLHACPCATQPYC 81
 DB 189 QSS-----CCKPCCCGSSC 202

RESULT 4

Q6D141 PRELIMINARY; PRT; 195 AA.
 AC Q6D141;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE 18 days embryo cDNA, RIKEN full-length enriched library,
 DE clone:1110030N11, full insert sequence.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxId=10090;
 RN NCB1 (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aikawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kato K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,
 RA Kuhl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schirini L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barab G.,
 RA Blake J., Boffelli D., Bojunga N., Carlini P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guenichon S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzaletti J., Mombaerts P.,

Db 128 SSCCKPCSSSGGSS---CCQSSCKPC 154

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Euthera; Primates; Carnivora; Homnidae; Homo.
OX NCBI_TaxId=9606;

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SCALP;
 RA Rogers M.A., Langbein L., Winter H., Ehmann C., Korn B., Schweizer J.;
 RT "Characterization of a cluster of human high/ultrahigh keratin
 associated proteins on chromosome 17q12-21."
 RL Submitted (OCT-2000) to the EMBL/Genbank/DBD databases.
 DR EMBL; AJ406934; CAC27573.1; -
 DR InterPro; IPR002494; Keratin B2.
 DR InterPro; IPR001368; TNFR_C6.
 DR Pfam; PF01500; Keratin B2; 1.
 DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
 SQ SEQUENCE 136 AA; 14402 MW; 51B51463925E02E CRC64;

Query Match 18.4%; Score 91.5; DB 4; Length 136;
 Best Local Similarity 29.7%; Pred. No. 0.00079;
 Matches 27; Conservative 5; Mismatches 38; Indels 21; Gaps 5;

QY 10 LHAACP--COLRC-----SSNTPLTQRYCCFYDSLHAC--PCLR---C 50
 DB 17 LENCPCPSCCQTTCCRTCCRPSCCVSSCCRPCCQSCQVCCQPTCCSCCQTTCCRTCC 76
 QY 51 SPPTQYCCFHSFYFDSLHACPPATCOPYC 81
 DB 77 RSCCVSSCFRPCCQSV--CCQPTCCRPSC 105

RESULT 8

Q9BYR2 PRELIMINARY; PRT; 186 AA.

DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Keratin associated protein 4.5.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SCALP;
 RA Rogers M.A., Langbein L., Winter H., Ehmann C., Korn B., Schweizer J.;
 RT "Characterization of a cluster of human high/ultrahigh keratin
 associated proteins on chromosome 17q12-21."
 RL Submitted (OCT-2000) to the EMBL/Genbank/DBD databases.
 DR EMBL; AJ406937; CAC27576.1; -
 DR InterPro; IPR002494; Keratin B2.
 DR InterPro; IPR001304; Lectin C.
 DR InterPro; IPR001368; TNFR_C6.
 DR InterPro; IPR001007; VWF_C.
 DR Pfam; PF01500; Keratin B2; 1.
 DR PROSITE; PS00615; C_TYFE_LECTIN_1; UNKNOWN_1.
 DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE; PS01208; VWF_C; UNKNOWN_2.
 SQ SEQUENCE 186 AA; 19916 MW; 034D9C7343D4F63A CRC64;

Query Match 18.4%; Score 91.5; DB 4; Length 186;
 Best Local Similarity 30.5%; Pred. No. 0.001;
 Matches 25; Conservative 6; Mismatches 28; Indels 23; Gaps 6;

QY 10 LHAACP--COLRCSNT--PPLTCQRYCCFYDSLHACPCRLCSPPTC-----QYCC 59
 DB 17 LENCPCPSCCQTTCCRTCCRPSCCVSSCCRPCCQSCQVCCQPTCCSCCQTTCCRTCC 71
 QY 60 FHSFYFDSLHACPPATCOPYC 81
 DB 72 FHS-----CCRPCCRPSC 85

RESULT 9
 064526

ID 064526 PRELIMINARY; PRT; 186 AA.

AC 064526;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Ultra-high sulphur keratin.

GN KRTAP9-1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCB1_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89140394; PubMed=2465353;

RA McNab A.R., Wood L., Threlkelt N., Gierman T., Vogel G.;

RT "An ultra-high sulfur keratin gene is expressed specifically during

hair growth".

RL J. Invest. Dermatol. 92:263-266(1989).

CC -1. SIMILARITY: TO THE PLANT THIONIN FAMILY.

DR EMBL; M27685; AAA81560.1; -

DR MGD; MGI:130997; Krtap9-1.

DR InterPro; IPR002494; Keratin B2.

DR InterPro; IPR001010; Thionin.

DR InterPro; IPR001368; TNFR_C6.

DR InterPro; IPR001007; VWF_C.

DR Pfam; PF01500; Keratin B2; 1.

DR PROSITE; PS00271; THIONIN; 1.

DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.

DR PROSITE; PS01208; VWF_C; UNKNOWN_1.

SQ SEQUENCE 186 AA; 19658 MW; 61D6BDBA72CFEB4 CRC64;

Query Match 18.4%; Score 91.5; DB 11; Length 186;
 Best Local Similarity 34.7%; Pred. No. 0.001;
 Matches 25; Conservative 4; Mismatches 24; Indels 19; Gaps 6;

QY 14 CTP--COLRC--SSNTPLTQRYCCFYDSLHAC--PCLRSPPTQYCCFHSFYDSL 69
 DB 85 CQPCQPCSCCQSCQPCRCSSCCQPCRCISSCCQPC--CRPSCQSSC----- 132
 QY 70 HACPPATCOPYC 81
 DB 133 --CRPC--CQPC 141

RESULT 10

Q9D3H7 PRELIMINARY; PRT; 191 AA.

DT 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE 10 days neonate head cDNA, RIKEN full-length enriched library,

clone:5530401L02, full insert sequence.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCB1_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=HEAD;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Aikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schirral L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Oikido T., Furuno M., Aono H., Baldarelli R., Barab G.,

RA Blake J., Boffelli D., Bojunga N., Carmine P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Guentrich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Marzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shihata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,
 RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlschki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL; AK017437; BAB30743.1; -
 DR InterPro; IPR002494; Keratin_B2.
 DR InterPro; IPR001010; Thionin.
 DR InterPro; IPR001368; TNFR_c6.
 DR InterPro; IPR001007; VWF_C.
 DR Pfam; PF01500; Keratin_B2; 1.
 DR PROSITE; PS00271; THIONIN; UNKNOWN_1.
 DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE; PS01208; VWF; UNKNOWN_1.
 SQ SEQUENCE 191 AA; 2008 MW; 522B841DC9A8A9D5 CRC64;

Query Match 18.4%; Score 91.5; DB 11; Length 191;
 Best Local Similarity 32.9%; Pred. No. 0.0011;
 Matches 23; Conservative 3; Mismatches 21; Indels 23; Gaps 5;

OY 16 PCQLACSSNTP---PLTCORYCCFHFDSILHACPCRCSPPTCO-YCCFHSYFSLHMA 71
 DB 63 PCCVSSCCRTPCPCPCCCVSSCCQ-----PC--CQPSCCSCSCCQPS-----C 103

OY 72 CPATCOPYC 81
 DB 104 CQPSCCQPS 113

RESULT 11
 O9BYR3 PRELIMINARY; PRT; 159 AA.

ID O9BYR3
 AC O9BYR3
 DT 01-JUN-2001 (TRENBLrel. 17, Created)
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
 DT 01-OCT-2001 (TRENBLrel. 18, Last annotation update)
 DE Keratin associated protein 9.3.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SCALP;
 RA Rogers M.A., Langbein L., Winter H., Ehmann C., Korn B., Schweizer J.,
 RT "Characterization of a cluster of human high/ ultrahigh keratin
 RT associated proteins on chromosome 17q12-21."
 RL Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.

DR EMBL; AJ406947; CAC27586.1; -
 DR InterPro; IPR002494; Keratin_B2.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF01500; Keratin_B2; 1.
 DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
 SQ SEQUENCE 159 AA; 16853 MW; 375CC1E52BECB68 CRC64;

Query Match 17.9%; Score 89; DB 4; Length 159;
 Best Local Similarity 29.5%; Pred. No. 0.0018;
 Matches 26; Conservative 4; Mismatches 20; Indels 38; Gaps 7;

OY 10 LHAACIP-CQLAC-----SSNTPLTCORYCCFHFDSILHAC-PCRLCSP 53
 DB 1 MHNCSPCCQPTTCQRTTCQPTVTTCSSPT--CCQPSCT-----VSSCCQPC-CHPT 50

OY 54 TCQYCCFHSYFDSILHACPCATCOPYC 81
 DB 51 CCQNTC-----CRITCCQPCIC 66

RESULT 12

O88281
 ID O88281 PRELIMINARY; PRT; 1574 AA.

AC O88281
 DT 01-NOV-1998 (TRENBLrel. 08, Created)
 DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE MEGP6.

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
 RX MEDLINE=98360089; PubMed=9693030;
 RA Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.,
 RT "Identification of high-molecular-weight proteins with multiple EGF-
 RT like motifs by motif-trap screening."
 RL Genomics 51:27-34(1998).

DR EMBL; AB011532; BAA32462.1; -
 DR HSSP; P00736; IAPQ.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001881; EGF_Ca.

DR Pfam; PF00008; EGF_24.
 DR SMART; SM00179; EGF_CA; 4.
 DR SMART; SM00001; EGF-like; 19.
 DR PROSITE; PS00010; ASX_HYDROXYL; 5.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_23.
 DR PROSITE; PS01186; EGF_2; 23.
 DR PROSITE; PS01187; EGF_CA; 5.

DR KX Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
 SQ SEQUENCE 1574 AA; 165445 MW; 2B4853D8F776E7 CRC64;

Query Match 17.9%; Score 89; DB 11; Length 1574;
 Best Local Similarity 29.4%; Pred. No. 0.014;
 Matches 30; Conservative 9; Mismatches 25; Indels 38; Gaps 8;

OY 1 CSQNYFDSILHACIPQCL-----RCSNTPLT-----CQRCCEY-----PDSILHACPC 47
 DB 966 CSAGAPCDVAVTGSCI-CPAGRWGRPCQSCPLTYGLNCSQCTCFNAGACDSVTGQC-- 1022

OY 48 LRCSF-----PTCQYCCFHSYFDSILHACPPA---TCQPYC 81
 DB 1023 -HCARGMGPTC-----LQACPEGLYKNCQHC 1050

RESULT 13
 O9BYR3 PRELIMINARY; PRT; 166 AA.

ID O9BYR3
 AC O9BYR3
 DT 01-JUN-2001 (TRENBLrel. 17, Created)
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
 DE Keratin associated protein 4.4.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SCALP;
 RA Rogers M.A., Langbein L., Winter H., Ehmann C., Korn B., Schweizer J.,
 RT "Characterization of a cluster of human high/ ultrahigh keratin
 RT associated proteins on chromosome 17q12-21."
 RL Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.

DR EMBL; AJ406936; CAC27575.1; -
 DR InterPro; IPR002494; Keratin_B2.
 DR InterPro; IPR001368; TNFR_c6.
 DR InterPro; IPR001007; VWF_C.
 DR Pfam; PF01500; Keratin_B2; 1.

DR InterPro; IPR001368; TNFR_c6.
 DR InterPro; IPR001007; VWF_C.
 DR Pfam; PF01500; Keratin_B2; 1.

DR PROSITE; PS00652; TNFR_NGFR.1; UNKNOWN.1.
 DR PROSITE; PS01208; VMP; UNKNOWN.1.
 SQ SEQUENCE 166 AA; 18023 MW; 1C37D121611A7115 CRC64;

Query Match 17.7%; Score 88; DB 4; Length 166;
 Best Local Similarity 28.4%; Pred. No. 0.0025; Indels 30; Gaps 5;
 Matches 25; Conservative 4; Mismatches 29;

QY 10 LHAACIP--COLRC-----SSNTPPLTCQRYCCFYDLSLHACPCUR--CSP 53
 DB 17 LENCGRPSYQTTTCRTTCRPSGCVSSCCRPCCQTTCCR--TTCCHPSCVSSCCRPQ 74

QY 54 TCQYCCFHSFYDLSLHACPPATCQPYC 81
 DB 75 CCQSV-----CQPTCCRPQC 90

RESULT 14

ID Q9BYQ2 PRELIMINARY; PRT; 154 AA.

AC Q9BYQ2; 01-JUN-2001 (TRENBLREL. 17, Created)

DT 01-JUN-2001 (TRENBLREL. 17, Last sequence update)

DE Keratin associated protein 9.4.

GN KRTAP9.4.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=SCALP;

RA Rogers M.A., Langbein L., Winter H., Ehmann C., Korn B., Schweizer J.,

RT "Characterization of a cluster of human high/ultrahigh keratin

RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ406948; CAC27587.1; -

DR InterPro; IPR002494; Keratin B2.

DR Pfam; PF01500; Keratin B2; 1

SQ SEQUENCE 154 AA; 16454 MW; 2EAF862E16165105 CRC64;

Query Match 17.6%; Score 87.5; DB 4; Length 154;
 Best Local Similarity 26.4%; Pred. No. 0.0027;
 Matches 29; Conservative 10; Mismatches 30; Indels 41; Gaps 8;

QY 1 CSQNEFYD--SLHACIP-----COLRC-----SSNTPPLTCQRYCCFYDLS 40
 DB 56 CCQNTCCQPTCVTSCCPSCSTPCQPTCCGSSCDQSSCAVYCRKTC--YPTTVCL 113

QY 41 ---LHAAC-----PCLRCSPPTCQYCCFHSFYDLSLHACPPATCQPYC 81
 DB 114 PGLNCSGCSNCCQPC--CRPACCTTCFP-----TCVYSCQPC 153

RESULT 15

ID Q9BYQ4 PRELIMINARY; PRT; 174 AA.

AC Q9BYQ4; 01-JUN-2001 (TRENBLREL. 17, Created)

DT 01-JUN-2001 (TRENBLREL. 17, Last sequence update)

DE Keratin associated protein 9.2.

GN KRTAP9.2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=SCALP;

RA Rogers M.A., Langbein L., Winter H., Ehmann C., Korn B., Schweizer J.,

RT "Characterization of a cluster of human high/ultrahigh keratin

RT associated proteins on chromosome 17q12-21."
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ406946; CAC27585.1; -
 DR InterPro; IPR002494; Keratin B2.
 DR Pfam; PF01500; Keratin B2; 1

SQ SEQUENCE 174 AA; 18261 MW; 2C378CFB0AA9F24D CRC64;
 Query Match 17.6%; Score 87.5; DB 4; Length 174;
 Best Local Similarity 28.6%; Pred. No. 0.003;
 Matches 26; Conservative 4; Mismatches 22; Indels 39; Gaps 7;

QY 10 LHAACIP--COLACSSNT-----PPLT-----CQRYCCFYDLSLHAC--PCLRC 50
 DB 1 WTRCSPCCQPTTCRTTCRTTCWKRPVTYTCSTSTSCQPACC-----VSSCCQPC--C 52

QY 51 SPPTCQYCCFHSFYDLSLHACPPATCQPYC 81
 DB 53 RPTSCQNTC-----CRTCCQPTC 71

Search completed: February 4, 2003, 12:59:08
 Job time : 18.3806 secs

GenCore version 5.1.3
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OM protein - protein search, using SW model

Run on: February 4, 2003, 12:53:16 ; Search time 5.5749 Seconds
(without alignments)
602.627 Million cell updates/sec

Title: US-09-854-864-13

Perfect score: 498
Sequence: 1 CSQNEKFDLSLHACIPQLR.....SEYFDSLHACPPATCPYC 81

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-------------|--------------------|
| 1 | 201 | 40.4 | 184 | TR17_HUMAN | Q02223 homo sapien |
| 2 | 136 | 27.3 | 185 | TR17_MOUSE | O86472 mus musculu |
| 3 | 98 | 19.7 | 249 | T13X_MOUSE | Q96c35 mus musculu |
| 4 | 93 | 18.7 | 293 | T13X_HUMAN | O14836 homo sapien |
| 5 | 92.5 | 18.6 | 169 | KRUA_HUMAN | P26371 homo sapien |
| 6 | 91 | 18.3 | 194 | KRUB_HUMAN | O76990 homo sapien |
| 7 | 87 | 17.5 | 1680 | PUR2_DROME | P34432 drosophila |
| 8 | 86.5 | 17.4 | 1877 | PCRS_MOUSE | Q04592 mus musculu |
| 9 | 83 | 16.7 | 131 | KRA3_SHEEP | P02441 ovls aries |
| 10 | 82 | 16.5 | 526 | UBPW_MOUSE | Q61068 mus musculu |
| 11 | 81 | 16.3 | 1587 | LMG3_HUMAN | O61415 mus musculu |
| 12 | 80.5 | 16.2 | 937 | PAC4_RAT | O61415 rattus norv |
| 13 | 80.5 | 16.2 | 1798 | LMB2_HUMAN | P55268 homo sapien |
| 14 | 80 | 16.1 | 3075 | LMW1_HUMAN | P25391 homo sapien |
| 15 | 79.5 | 16.0 | 965 | YNC3_YEAST | P53971 saccharomyc |
| 16 | 79.5 | 16.0 | 3133 | HMCT_BOVMO | P98092 bombyx mori |
| 17 | 79 | 15.9 | 1696 | PCK5_BACUL | O9n115 branchiost |
| 18 | 77.5 | 15.6 | 132 | KRA3_CAPRI | P03442 capra hircu |
| 19 | 77.5 | 15.6 | 139 | SPY1_HUMAN | O43609 homo sapien |
| 20 | 77 | 15.5 | 171 | KRA2_SHEEP | P02441 ovls aries |
| 21 | 77 | 15.5 | 5376 | ZAN_MOUSE | O86799 mus musculu |
| 22 | 76.5 | 15.4 | 2414 | P300_HUMAN | Q04972 homo sapien |
| 23 | 76 | 15.3 | 2441 | CBP_MOUSE | P45481 mus musculu |
| 24 | 75.5 | 15.2 | 1713 | LMW3_HUMAN | O16787 homo sapien |
| 25 | 75 | 15.1 | 1581 | LMW3_MOUSE | Q970b6 mus musculu |
| 26 | 75 | 15.1 | 1609 | LMG1_HUMAN | P11047 homo sapien |
| 27 | 74.5 | 15.0 | 610 | CABP_BOVIN | Q02865 bos taurus |
| 28 | 74 | 14.9 | 1786 | LMW1_HUMAN | P07942 homo sapien |
| 29 | 74 | 14.9 | 2442 | CBP_HUMAN | Q94793 mus musculu |
| 30 | 73.5 | 14.8 | 313 | SPY1_MOUSE | O61292 mus musculu |
| 31 | 73.5 | 14.8 | 1799 | LMW2_MOUSE | O61292 mus musculu |
| 32 | 72.5 | 14.6 | 969 | PAC4_HUMAN | P26122 homo sapien |
| 33 | 72.5 | 14.6 | 1592 | SORTL_CHICK | Q09930 g sortilin- |

| | | | | | | |
|----|------|------|------|---|------------|--------------------|
| 34 | 72 | 14.5 | 575 | 1 | TRBM_HUMAN | P07204 homo sapien |
| 35 | 72 | 14.5 | 867 | 1 | SPPO_BOVIN | P98167 bos taurus |
| 36 | 72 | 14.5 | 1367 | 1 | IGIR_HUMAN | P08069 homo sapien |
| 37 | 72 | 14.5 | 1700 | 1 | BAR3_CHITR | Q03376 chironomus |
| 38 | 72 | 14.5 | 2569 | 1 | LMW3_MOUSE | O61789 mus musculu |
| 39 | 72 | 14.5 | 4655 | 1 | LRP2_HUMAN | P98164 homo sapien |
| 40 | 71.5 | 14.4 | 1435 | 1 | EBAL_PLAFC | P19214 plasmodium |
| 41 | 71 | 14.3 | 62 | 1 | IBB_MEDSC | P80321 medicago sc |
| 42 | 71 | 14.3 | 63 | 1 | ICE1_ASCSU | P07851 ascaris suu |
| 43 | 71 | 14.3 | 810 | 1 | NEI1_HUMAN | Q92832 homo sapien |
| 44 | 71 | 14.3 | 3712 | 1 | IMA_DROME | O00174 drosophila |
| 45 | 70.5 | 14.2 | 96 | 1 | IBB1_PEA | Q41065 pisum sativ |

ALIGNMENTS

| RESULT 1 | ID | TR17_HUMAN | STANDARD; | PRT; | 184 AA. |
|----------|--|-----------------------------------|-----------|------|---------|
| AC | Q02223; | | | | |
| DT | 01-JUN-1993 | (Rel. 26, Created) | | | |
| DT | 01-JUN-1993 | (Rel. 26, Last sequence update) | | | |
| DT | 15-JUN-2002 | (Rel. 41, Last annotation update) | | | |
| DE | Tumor necrosis factor receptor superfamily member 17 (B-cell maturation protein). | | | | |
| GN | TNFRSF17 OR BCMA OR BCM. | | | | |
| OS | Homo sapiens (Human). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | | |
| OX | NCBI_TaxID=9606; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A., AND CHROMOSOMAL TRANSLOCATION. | | | | |
| RC | Tissue=Peripheral blood leukocytes, and Lymph node; | | | | |
| RX | MEDLINE=93010984; PubMed=1396583; | | | | |
| RA | Laabli Y., Gras M.P., Cardonnel F., Brouet J.C., Berger R., Larsen C.J., Tsapis A.; | | | | |
| RT | "A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a c(4;16)(q26;p13) translocation in a malignant T cell lymphoma."; | | | | |
| RL | EMBO J. 11:3897-3904(1992). | | | | |
| RN | [2] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RX | MEDLINE=94218235; PubMed=8165126; | | | | |
| RA | Laabli Y., Gras M.P., Brouet J.C., Berger R., Larsen C.J., Tsapis A.; | | | | |
| RT | "The BCMA gene, preferentially expressed during B lymphoid maturation, is bidirectionally transcribed."; | | | | |
| RL | Nucleic Acids Res. 22:1147-1154(1994). | | | | |
| RN | [3] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RX | MEDLINE=99425270; PubMed=10493829; | | | | |
| RA | Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R., Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L., DeLattas M.A., Cao Y., Xu R.X., Kang H.-L., Mitchell S., Eichler E.E., Harris P.C., Venter J.C., Adams M.D.; | | | | |
| RT | "Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q."; | | | | |
| RL | Genomics 60:295-308(1999). | | | | |
| RN | [4] | | | | |
| RP | SEQUENCE FROM N.A., AND VARIANT THR-153. | | | | |
| RX | MEDLINE=21419161; PubMed=11528522; | | | | |
| RA | Kawasaki A., Tsuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.; | | | | |
| RT | "Presence of four major haplotypes in human BCMA gene: lack of association with systemic lupus erythematosus and rheumatoid arthritis."; | | | | |
| RL | Genes Immun. 2:276-279(2001). | | | | |
| RN | [5] | | | | |
| RP | FUNCTION. | | | | |
| RX | MEDLINE=20363816; PubMed=10903733; | | | | |
| RA | Hatzoglou A., Rousselet J., Bourgeade M.-F., Rogier B., Madry C., Inoue Y., Devigne O., Tsapis A.; | | | | |
| RT | "TNF receptor family member BCMA (B cell maturation) associates with TNF receptor-associated factor (TRAF) 1, TRAF2, and TRAF3 and activates NF-kappa B, elk-1, c-Jun N-terminal kinase, and p38 | | | | |

RT mitogen-activated protein kinase.";
 RL J. Immunol. 165:1322-1330(2000).
 RP FUNCTION.
 RX MEDLINE=20259066; PubMed=10801128;
 RA Gross J.A., Johnston J., Mudri S., Enselman R., Dillon S.R.,
 RA Madden K., Xu W., Parrish-Novak J., Foster D., Lofton-Day C.,
 RA Moore W., Little A., Grossman A., Haugen H., Foley K., Blumberg H.,
 RA Harrisson K., Kindevogel W., Clegg C.H.;
 RA "TACI and BCMA are receptors for a TNF homologue implicated in B-cell
 RT autoimmune disease.";
 RT Nature 404:995-999(2000).
 RL Nature 404:995-999(2000).
 RN [7]
 RP FUNCTION, AND INTERACTION WITH APRIL AND BAFF.
 RX MEDLINE=21170294; PubMed=10973284;
 RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
 RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
 RA Boyle W.J., Sarosi I., Heu H., Senaldi G., Thell L.E.;
 RA "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating
 RT humoral immunity.";
 RT Nat. Immunol. 1:252-256(2000).
 RL [8]
 RP INTERACTION WITH TRAF5 AND TRAF6.
 RX MEDLINE=20381353; PubMed=10908663;
 RA Shu H.-B., Johnson H.;
 RT "B cell maturation protein is a receptor for the tumor necrosis factor
 RT family member TALL-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).
 CC -1- FUNCTION: Receptor for TNFSF13B/BLYS/BAFF and TNFSF13/APRIL.
 CC Promotes B-cell survival and plays a role in the regulation of
 CC humoral immunity. Activates NF-kappa-B and JNK.
 CC -1- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein. Plasma membrane
 CC and perinuclear Golgi-like structures.
 CC -1- TISSUE SPECIFICITY: Expressed in mature B-cells, but not in T-
 CC cells or monocytes.
 CC -1- DISEASE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL) IS
 CC CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(4;16)(Q26;P13)
 CC WHICH INVOLVES BCMA AND IL2.
 CC -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC DR EMBL, 214954; CAA78679.1; -;
 CC DR EMBL, 229575; CAA82691.1; -;
 CC DR EMBL, 229574; CAA82690.1; -;
 CC DR EMBL, U95742; AAB67251.1; -;
 CC DR EMBL, AB052772; BAB60895.1; -;
 CC DR PIR, S31208; S31208.
 CC DR PIR, S31209; S31209.
 CC DR Genew; HGNC:11913; TNFRSF17.
 CC DR MIM; 109545; -;
 CC KW Receptor; Immune response; Proto-oncogene; Signal-anchor;
 CC Transmembrane; Chromosomal translocation; Polymorphism.
 CC FT DOMAIN 1 54
 CC FT TRANSMEM 55 77
 CC FT SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
 CC FT (POTENTIAL).
 CC FT CYTOPLASMIC (POTENTIAL).
 CC FT TNFR-CYS
 CC FT REPEAT 7 184
 CC FT SITE 3 4
 CC FT DISULFID 8 21
 CC FT DISULFID 24 37
 CC FT DISULFID 28 41
 CC FT VARIANT 153 153
 CC FT A->T.
 CC FT SEQUENCE, 184 AA; 20138 MW; 277AF11E2767D932 CRC64;

Query Match 40.4%; Score 201; DB 1; Length 184;
 Best Local Similarity 100.0%; Pred. No. 4.2e-13;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CSQNEFYDLSLHACIPQCLRCSSNTPPLTCORYC 34
 DB 8 CSQNEFYDLSLHACIPQCLRCSSNTPPLTCORYC 41
 RESULT 2
 TR17_MOUSE STANDARD; PRT; 185 AA.
 AC 088472;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 17 (B-cell
 DE maturation protein).
 GN TNFRSF17 OR BCMA OR BCM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=BALB/c; TISSUE=Spleen;
 RX MEDLINE=99061155; PubMed=9846698;
 RA Madry C., Laabi Y., Callebaut I., Rousset J., Hatzoglou A.,
 RA Le Coniat M., Morion J.P., Berger R., Tsapis A.;
 RT "The characterization of murine BCMA gene defines it as a new member
 RL of the tumor necrosis factor receptor superfamily.";
 RL Int. Immunol. 10:1693-1702(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Akawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schmitt L.M., Stebbi F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barb G.,
 RA Blake J., Boffelli D., Bojunga N., Carinci P., de Bona M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohcenki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -1- FUNCTION: Receptor for TNFSF13B/BLYS/BAFF and TNFSF13/APRIL.
 CC Promotes B-cell survival and plays a role in the regulation of
 CC humoral immunity. Activates NF-kappa-B and JNK (by similarity).
 CC -1- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
 CC produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: Detected in spleen, thymus, bone marrow and
 CC heart, and at lower levels in kidney and lung.
 CC -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
 CC -----
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 CC -----
 DR EMBL; AF061505; AAC23799.1; -
 DR EMBL; AK020247; BAB2038.1; -
 DR MGI; MGI:1343050; Tnfra17.
 KW Receptor; Immune response; Signal-anchor; Transmembrane;
 KW Alternative splicing.
 FT DOMAIN 1
 FT TRANSMEM 50
 FT SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT REPEAT 71
 FT 185
 FT BY SIMILARITY.
 FT DISULFID 5
 FT 18
 FT BY SIMILARITY.
 FT DISULFID 21
 FT 32
 FT BY SIMILARITY.
 FT DISULFID 25
 FT 36
 FT MISSING (IN ISOFORM 2).
 FT VARSPLIC 87
 FT 91
 FT 20442 MW; 880635284FD26ABE CRC64;
 FT SEQUENCE 185 AA;
 Query Match 27.3%; Score 136; DB 1; Length 185;
 Best Local Similarity 70.6%; Pred. No. 8.1e-07;
 Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;
 Qy 1 CSQNEYPDSLHACIPCOLRGSSNTPPTQRYC 34
 Db 5 CFHSYFDSLHACIPKCHLRCSN--PPATCOPYC 36
 RESULT 3
 ID 113X MOUSE STANDARD; PRT; 249 AA.
 AC Q9ERT3; Q9EBZ3;
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane
 DE activator and CML interactor).
 GN TNFRSF13B OR TACI.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RX SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=21177254; PubMed=10881172;
 RA Yan M., Masters S.A., Grewal I.S., Wang H., Ashkenazi A.,
 RA Dixit V.M.;
 RT "Identification of a receptor for Bly's demonstrates a crucial role in
 RT humoral immunity."
 RL Nat. Immunol. 1:37-41(2000).
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Komoto H., Adachi Y., Fukuda S.,
 RA Atawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamada S.,
 RA Saito T., Okazaki Y., Gojohori T., Hono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischiemann W., Gasteierland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Penzo G., Quackenbush J.,
 RA Schirral L.M., Staehli F., Suzuki R., Tomita M., Wagner L., Maehio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Botfield D., Boujunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guettich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombere P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakano N.,
 RA Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Winking L.,
 RA Wyshaw-Boris A., Yoshida K., Haegawa Y., Kawai H., Kohsaki S.,

RA Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 RN [3]
 RP FUNCTION.
 RX MEDLINE=20341628; PubMed=10880535;
 RA Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,
 RA Theil L.E., Colombero A., Solovayev I., Lee F., McCabe S., Elliott R.,
 RA Miner K., Hawkins N., Guo J., Stolna M., Yu G., Wang J., Delaney J.,
 RA Meng S.-Y., Boyle W.J., Han H.;
 RT "TRAC1 is a TRAF-interacting receptor for TALL-1, a tumor necrosis
 RT factor family member involved in B cell regulation."
 RL J. Exp. Med. 192:137-143(2000).
 RN [4]
 RP FUNCTION.
 RX MEDLINE=21322748; PubMed=11429548;
 RA Wang H., Masters S.A., Baker T., Chan B., Lee W.P., Fu L., Tumas D.,
 RA Yan M., Dixit V.M., Ashkenazi A., Grewal I.S.;
 RT "TRAC1-ligand interactions are required for T cell activation and
 RT collagen-induced arthritis in mice."
 RL Nat. Immunol. 2:632-637(2001).
 CC -1- FUNCTION: Receptor for TNFRSF13/APRIL and TNFRSF13B/TALL1/BAFF/BLYS
 CC that binds both ligands with similar high affinity. Mediates
 CC calcineurin-dependent activation of NF-AT, as well as activation
 CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
 CC cell function and the regulation of humoral immunity (by
 CC similarity).
 CC -1- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
 CC domain of CMT6 with its C-terminus (by similarity).
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
 CC -1- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
 CC
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 CC -----
 DR EMBL; AF257673; AAG00081.1; -
 DR EMBL; AK004668; BAB23457.1; -
 DR MGI; MGI:1889411; Tnfra13b.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS50050; TNFR_NGFR_2; 2.
 KW Receptor; Immune response; Signal-anchor; Transmembrane; Repeat.
 FT DOMAIN 1
 FT TRANSMEM 129
 FT SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT REPEAT 5
 FT 249
 FT BY SIMILARITY.
 FT DISULFID 6
 FT 19
 FT BY SIMILARITY.
 FT DISULFID 22
 FT 34
 FT BY SIMILARITY.
 FT DISULFID 26
 FT 38
 FT BY SIMILARITY.
 FT DISULFID 43
 FT 58
 FT BY SIMILARITY.
 FT DISULFID 61
 FT 72
 FT BY SIMILARITY.
 FT DISULFID 65
 FT 76
 FT BY SIMILARITY.
 FT CONFLICT 137
 FT 137
 FT I -> F (IN REF. 2).
 FT SEQUENCE 249 AA; 26947 MW; CB2F2D61C2931B81 CRC64;
 Query Match 19.7%; Score 98; DB 1; Length 249;
 Best Local Similarity 25.6%; Pred. No. 0.0049;
 Matches 22; Conservative 12; Mismatches 27; Indels 28; Gaps 4;
 Qy 1 CSQNEYPDSLHACIPCOLRGSSNTPPTQRYCCEYFDSLHACIPCLRCSPPTQYCCF 60
 Db 6 CPKQYDMSRKSCVSCALTRCSGRS-----QRTCTDF-----CKFLNCRKE----- 46
 Qy 61 HSEYFDSLHAC-----PPATCOPYC 81
 Db 47 QGRYYDHLGACVSCDSTCTQHPOOAHFC 76

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RESULT 4
ID T13X_HUMAN STANDARD; PRT; 293 AA.
AC 014836;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane
DE activator and CAML interactor).
GN TNFRSF13B OR TACI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA MEDLINE=97458245; PubMed=9311921;
RT "NF-AT activation induced by a CAML-interacting member of the tumor
RT necrosis factor receptor superfamily.";
RL Science 278:138-141(1997).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strusberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
[3]
RP FUNCTION.
RA MEDLINE=20519647; PubMed=10956646;
RA Wu Y., Bressette D., Carrell J.A., Kaufman T., Feng P., Taylor K.,
RA Gan Y., Cho Y.H., Garcia A.D., Gollatz E., Dimke D., Lafleur D.,
RA Migone T.S., Nardelli B., Wei P., Ruben S.M., Ullrich S.J.,
RA Olsen H.S., Kanakara P., Moore P.A., Baker K.P.;
RT "Tumor necrosis factor (TNF) receptor superfamily member TACI is a
RT high affinity receptor for TNF family members APRIL and BLys.";
RL J. Biol. Chem. 275:35478-35485(2000).
[4]
RP FUNCTION.
RA MEDLINE=21170294; PubMed=10973284;
RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
RA McCabe S., Qiu W.R., Korum M., Xia X.-Z., Guo J., Stolima M.,
RA Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;
RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating
RT humoral immunity.";
RL Nat. Immunol. 1:252-256(2000).
[5]
RP FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAFF/BLYS
RP that binds both ligands with similar high affinity. Mediates
RP calcineurin-dependent activation of NF-kappa-B, as well as activation
RP of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
RP cell function and the regulation of humoral immunity.
CC -1- SUBUNIT: Binds TRAF2, TRAF3 and TRAF6. Binds the NH2-terminal
CC domain of CAML with its C-terminus.
CC -1- SUBCELLULAR LOCATION: Type III membrane protein.
CC -1- TISSUE SPECIFICITY: Highly expressed in spleen, thymus, small
CC intestine and peripheral blood leukocytes. Expressed in resting B-
CC cells and activated T-cells, but not in resting T-cells.
CC -1- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
CC -1- CAUTION: It is uncertain whether Met-1 or Met-31 is the initiator.
CC -----
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CC -----
CC EMBL; AF023614; AAC51790.1; -
CC EMBL; BC028072; AAH28072.1; -
CC DR EMBL; HGNC:18153; TNFRSF13B.
CC MIM; 604907; -.

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DR InterPro, IPR001368; TNFR_C6.
DR PROSITE, PS00652; TNFR_NGFR_1; 1.
DR PROSITE, PS50050; TNFR_NGFR_2; FALSE NEG.
KW Receptor; Immune response; Signal-anchor; Transmembrane; Glycoprotein;
KW Repeat.
FT DOMAIN 1 165 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 166 186 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
FT DOMAIN 187 293 CYTOPLASMIC (POTENTIAL).
FT REPEAT 33 67 TNFR-CYS 1.
FT REPEAT 70 104 TNFR-CYS 2.
FT DISULFID 34 47 BY SIMILARITY.
FT DISULFID 50 62 BY SIMILARITY.
FT DISULFID 54 66 BY SIMILARITY.
FT DISULFID 71 86 BY SIMILARITY.
FT DISULFID 89 100 BY SIMILARITY.
FT DISULFID 93 104 BY SIMILARITY.
FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 251 251 P -> L (IN REF. 2).
SQ SEQUENCE 293 AA; 31816 MW; 411799F3DE17A5EB CRC64;

Query Match 18.7%; Score 93; DB 1; Length 293;
Best Local Similarity 28.4%; Pred. No. 0.017;
Matches 21; Conservative 13; Mismatches 22; Indels 18; Gaps 5;

QY 1 CSQNEYFDSLHACIPQGLRCSNTPTTCQRYC-----EYFDSLHACPCQLRCS 51
DB 34 CPBEGYMPPLLTGTCMCKTICNHQS-QRTCAAFGRSLSCREKGKFDYHLRR--DCISCA 90
QY 52 -----PPTCQYCC 59
DB 91 SICGHPKQCAVFC 104

RESULT 5
ID KRUA_HUMAN STANDARD; PRT; 169 AA.
AC P26371;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Keratin, ultra high-sulfur matrix protein A (UHS keratin A) (UHS
DE KeraA).
GN KRN1 OR UHSK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RP TISSUE=follicle;
RA MEDLINE=9115951; PubMed=1703541;
RA McKinnon P.J., Powell B.C., Rogers G.E.;
RT "Structure and expression of genes for a class of cysteine-rich
RT proteins of the cuticle layers of differentiating wool and hair
RT follicles.";
RL J. Cell Biol. 111:2587-2600(1990).
[2]
RP SEQUENCE FROM N.A.
RP MEDLINE=99148005; PubMed=10023043;
RA Perez C., Auriol J., Gerst C., Bernard B.A., Egly J.-M.;
RT "Genomic organization and promoter characterization of two human UHS
RT keratin genes.";
RL Gene 227:137-148(1999).
[3]
RP FUNCTION: THE KERATIN PRODUCTS OF MAMMALIAN EPIDERMAL DERIVATIVES
RP SUCH AS WOOL AND HAIR CONSIST OF MICROFIBRILS EMBEDDED IN A RIGID
RP MATRIX OF OTHER PROTEINS. THE MATRIX PROTEINS INCLUDE THE HIGH-
RP SULFUR AND HIGH-TYROSINE KERATINS, HAVING MOLECULAR WEIGHTS OF
RP 6-20 kDa, WHEREAS THE MICROFIBRILS CONTAIN THE LARGER, LOW-SULFUR
RP KERATINS (40-56 kDa).
CC -1- TISSUE SPECIFICITY: CUTICLE LAYERS OF DIFFERENTIATING
CC HAIR FOLLICLES.
CC -1- DEVELOPMENTAL STAGE: AT A LATE STAGE OF FIBER DIFFERENTIATION.

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CC -1- DOMAIN: MAINLY COMPOSED OF CYS-RICH (CR), GLY-RICH (GR) AND SER-
CC RICH (SR) REPEATS.
CC -1- SIMILARITY: BELONGS TO THE UHS KERATIN FAMILY.
CC -----
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CC -----
DR EMBL; X55293; CAA39005.1; -.
DR EMBL; AJ006693; CAA07189.1; -.
DR HSSP; P01064; 1P12.
DR Genew; HGNC:6409; KEN1.
DR MIT; 148021; -.
DR Keratin; Repeat; Multigene family.
DR SEQUENCE 169 AA; 16276 MW; 219B14FEEB49D4AB CRC64;
SQ
Query Match 18.6%; Score 92.5; DB 1; Length 169;
Best Local Similarity 30.0%; Pred. No. 0.012;
Matches 27; Conservative 5; Mismatches 37; Indels 21; Gaps 5;
QY 1 CSQNEYPDSLHACIPQCRSSNTPTTCQRYCCGYFDSLHAC-PCLR-----CS 51
DB 77 CSQ-----CSCKPC-CCSSGCGSSCCQCCCKPCYCSGSCCKPCSSSGSSCCQ 127
QY 52 PTCQYCCFHSEYFDSLHACPPATCQPYC 81
DB 128 SSCCKPCSSSGSS-----CCSSCKPC 154
RESULT 6
KRUB_HUMAN STANDARD; PRT; 194 AA.
AC 075690;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Keratin, ultra high-sulfur matrix protein B (UHS keratin B) (UHS
DE KerB).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99148005; PubMed=10023043;
RA Perez C., Aurioi J., Gerst C., Bernard B.A., Egly J.-M.;
RT "Genomic organization and promoter characterization of two human UHS
RT keratin genes.";
RT Gene 227:137-148(1999).
CC -1- FUNCTION: THE KERATIN PRODUCTS OF MAMMALIAN EPIDERMAL DERIVATIVES
CC SUCH AS WOOL AND HAIR CONSIST OF MICROFIBRILS EMBEDDED IN A RIGID
CC MATRIX OF OTHER PROTEINS. THE MATRIX PROTEINS INCLUDED THE HIGH-
CC SULFUR AND HIGH-TYROSINE KERATIN, HAVING MOLECULAR WEIGHTS OF
CC 6-20 kDa, WHEREAS THE MICROFIBRILS CONTRAIN THE LARGER, LOW-SULFUR
CC KERATINS (40-56 kDa).
CC -1- TISSUE SPECIFICITY: CUTICLE LAYERS OF DIFFERENTIATING
CC HAIR FOLLICLES
CC -1- DOMAIN: MAINLY COMPOSED OF CYS-RICH (CR), GLY-RICH (GR) AND SER-
CC RICH (SR) REPEATS.
CC -1- SIMILARITY: BELONGS TO THE UHS KERATIN FAMILY.
CC -----
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DR EMBL; AJ006692; CAA07188.1; -.
DR HSSP; P01055; 1B1.
DR Keratin; Repeat; Multigene family.
DR SEQUENCE 194 AA; 18094 MW; 8607B2AE90FE44A CRC64;
SQ
Query Match 18.3%; Score 91; DB 1; Length 194;
Best Local Similarity 31.7%; Pred. No. 0.019;
Matches 26; Conservative 6; Mismatches 26; Indels 24; Gaps 6;
QY 1 CSQNEYPDSLHACIPQCRSSNTPTTCQRYCCGYFDSLHACPCRCSPPT-CQYCC 59
DB 121 CSQSS-----CKPC-CCSSGCGSSCCQSSCK-----PC-CCSSCKPC 160
QY 60 FHSEYFDSLHACPPATCQPYC 81
DB 161 CSQCGSS-----CCQSSCKPC 179
RESULT 7
FUR2_DROME STANDARD; PRT; 1680 AA.
AC P30432;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-1998 (Rel. 36, Last annotation update)
DE Furin-like protease 2 precursor (EC 3.4.21.75) (Furin 2).
GN FUR2.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92381036; PubMed=1512259;
RA Roedbroek A.V.M., Creemers J.W.M., Pauli I.G.L., Kurzik-Dumke U.,
RA Rentrop M., Gateff B.A.F., Leunissen J.A.M., van de Ven W.J.;
RT "Cloning and functional expression of Dfurin2, a subtilisin-like
RT proprotein processing enzyme of Drosophila melanogaster with multiple
RT repeats of a cysteine motif.";
RT J. Biol. Chem. 267:17208-17215(1992).
CC -1- FUNCTION: FURIN IS LIKELY TO REPRESENT THE UBIQUITOUS ENDOPROTEASE
CC ACTIVITY WITHIN CONSTITUTIVE SECRETORY PATHWAYS AND CAPABLE OF
CC CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Release of mature proteins from their
CC proproteins by cleavage of Arg-Xaa-Yaa-Arg-|-Zaa bonds, where Xaa
CC can be any amino acid and Yaa is Arg or Lys. Releases albumin,
CC complement component C3 and von Willebrand factor from their
CC respective precursors.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8. FURIN SUBFAMILY.
CC -----
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CC -----
DR EMBL; M94375; AAA28551.1; -.
DR PIR; A43434; A43434.
DR HSSP; Q99405; 1MPT.
DR MEROPS; S08.049; -.
DR FLYBase; FBgn0004598; Fur2.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002174; Furin-like.
DR InterPro; IPR002884; P domain.
DR InterPro; IPR000209; Peptidase S8.
DR Pfam; PF00082; Peptidase S8; 1.
DR Pfam; PF01483; P; PARTIAL.
DR PRINTS; PR00723; SUBTILISIN.
DR PRODom; PD000717; P domain; 1.
DR SMART; SM00181; EGF; 1.

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DR SMART, SMO0261; FU, 10.
 DR PROSITE; PS00136; SUBTILASE ASP, 1.
 DR PROSITE; PS00137; SUBTILASE HIS, 1.
 DR PROSITE; PS00138; SUBTILASE SER, 1.
 KM Hydrolyase; Serine protease; Glycoprotein; signal; Transmembrane;
 KW Multigene family; Zymogen; Repeat
 FT SIGNAL 1
 FT PROPEP 1
 FT CHAIN 319
 FT ACT SITE 320 1680
 FT ACT SITE 418 418
 FT ACT SITE 457 457
 FT ACT SITE 638 638
 FT DOMAIN 962 1444
 FT REPEAT 962 1007
 FT REPEAT 1008 1057
 FT REPEAT 1058 1104
 FT REPEAT 1105 1153
 FT REPEAT 1154 1205
 FT REPEAT 1206 1254
 FT REPEAT 1255 1299
 FT REPEAT 1300 1346
 FT REPEAT 1347 1393
 FT REPEAT 1394 1444
 FT TRANSMEM 1508 1532
 FT DOMAIN 1533 1680
 FT CARBOHYD 3
 FT CARBOHYD 109 109
 FT CARBOHYD 130 130
 FT CARBOHYD 203 203
 FT CARBOHYD 443 443
 FT CARBOHYD 481 481
 FT CARBOHYD 928 928
 FT CARBOHYD 1061 1061
 FT CARBOHYD 1182 1182
 FT CARBOHYD 1275 1275
 FT CARBOHYD 1278 1278
 FT CARBOHYD 1440 1440
 SQ SEQUENCE 1680 AA; 183599 MW; 0A99CE8770A8E293 CRC64;
 Query Match 17.5%; Score 87; DB 1; Length 1680;
 Best Local Similarity 25.0%; Pred. No. 0.3; Mismatches 31; Indels 50; Gaps 9;
 Matches 31; Conservative 12; Mismatches 31; Indels 50; Gaps 9;
 QY 1 CSQNEFYDSLHACIPQQRCSNTPRLTQ--RYC--CEYFDSLH-----ACP---46
 DB 1051 CPDGYFENSRNRTVCPCENCAS-----CDHPXYCTSCDH-HLYMHKCYSAQPLDT 1103
 QY 47 -----CLRCSPPTCYC--CFHSYF--DSLHACPA-----TC 77
 DB 1104 YETEDNKKAFCHSTATCNGPTDQDCITCRSSRYAWQNKCLISCPDGYADKKRLCQMPG 1163
 QY 78 QPYC 81
 DB 1164 QEGC 1167
 RESULT 8
 PKCS MOUSE STANDARD; PRT; 1877 AA.
 AC Q04552; Q62040;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Proprotein convertase subtilisin/kexin type 5 precursor (EC 3.4.21.-)
 DE (Proprotein convertase PCS) (Subtilisin/kexin-like protease PCS)
 DE (Convertase PCS) (PCS) (Subtilisin-like proprotein convertase 6)
 DE (SP66).
 GN PCSK5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN [1]

RP SEQUENCE OF 330-1877 FROM N.A. (ISOFORM PCSB).
 RC STRAIN=ICR; TISSUE=Intestine;
 RX MEDLINE=93327934; PubMed=8335106;
 RA Nakagawa T., Murakami K., Nakayama K.;
 RT "Identification of an isoform with an extremely large Cys-rich region
 of PC6, a Kex2-like processing endoprotease.";
 RL FEBS Lett. 327:165-171(1993).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM PCSA).
 RC TISSUE=Brain, and Intestine;
 RX MEDLINE=93224489; PubMed=8468318;
 RA Nakagawa T., Hosaka M., Torii S., Watanabe T., Murakami K.,
 RA Nakayama K.;
 RT "Identification and functional expression of a new member of the
 mammalian Kex2-like processing endoprotease family: its striking
 structural similarity to PACE4.";
 RL J. Biochem. 113:132-135(1993).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM PCSA).
 RC TISSUE=Adrenal cortex;
 RX MEDLINE=93342056; PubMed=8341687;
 RA Lusson J., Vileau D., Hamelin J., Day R., Chretien M., Seidah N.G.;
 RT "cDNA structure of the mouse and rat subtilisin/kexin-like PCS: a
 candidate proprotein convertase expressed in endocrine and
 nonendocrine cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695(1993).
 RN [4]
 RP PARTIAL SEQUENCE, AND SUBCELLULAR LOCATION.
 RX MEDLINE=97103178; PubMed=8947550;
 RA De Bie I., Marcinkiewicz M., Malide D., Lazure C., Nakayama K.,
 RA Bendayan M., Seidah N.G.;
 RT "The isoforms of proprotein convertase PCS are sorted to different
 subcellular compartments.";
 RL J. Cell Biol. 135:1261-1275(1996).
 RN [5]
 RP DEVELOPMENTAL EXPRESSION.
 RX MEDLINE=96293359; PubMed=8698813;
 RA Constam D.B., Calton M., Robertson E.J.;
 RT "SPC4, SPC6, and the novel protease SPC7 are coexpressed with bone
 morphogenetic proteins at distinct sites during embryogenesis.";
 RL J. Cell Biol. 134:181-191(1996).
 RN [6]
 RP DEVELOPMENTAL EXPRESSION.
 RX MEDLINE=97436919; PubMed=9291583;
 RA Rancourt S.L., Rancourt D.E.;
 RT "Murine subtilisin-like proteasease SPC6 is expressed during embryonic
 implantation, somitogenesis, and skeletal formation.";
 RL Dev. Genet. 21:75-81(1997).
 CC -1- FUNCTION: LIKELY TO REPRESENT A WIDESPREAD ENDOPEPTIDASE ACTIVITY
 WITHIN THE CONSTITUTIVE AND REGULATED SECRETORY PATHWAY. CAPABLE
 OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF. MAY BE RESPONSIBLE
 FOR THE MATURATION OF GASTROINTESTINAL PEPTIDES. MAY BE INVOLVED
 IN THE CELLULAR PROLIFERATION OF ADRENAL CORTEX VIA THE ACTIVATION
 OF GROWTH FACTORS.
 CC -1- CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR
 PROPROTEINS BY CLEAVAGE OF ARG-XAA-YAA-ARG-|-ZAA BONDS, WHERE XAA
 CAN BE ANY AMINO ACID AND YAA IS ARG OR IYS.
 CC -1- SUBCELLULAR LOCATION: PCSA IS SECRETED THROUGH THE REGULATED
 SECRETORY PATHWAY. PCSB IS A TYPE I MEMBRANE PROTEIN LOCALIZED TO
 A PARANUCLEAR POST-GOLGI NETWORK COMPARTMENT IN COMMUNICATION WITH
 EARLY ENDOSOMES.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS, PCSB/LONG (SHOWN HERE)
 AND PCSA/SHORT; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: PCSA IS EXPRESSED IN MOST TISSUES BUT IS MOST
 ABUNDANT IN THE TESTES AND ADRENALS. PCSB IS EXPRESSED IN THE
 INTESTINE, ADRENALS AND LONG BUT NOT IN THE BRAIN.
 CC -1- DEVELOPMENTAL STAGE: WEAKLY EXPRESSED THROUGHOUT THE EMBRYO,
 EXCEPT IN THE DEVELOPING NERVOUS SYSTEM, THE LIVER AND THE LIVER,
 BUT MARKEDLY UPREGULATED AT DISCRETE SITES DURING DEVELOPMENT. AT
 E6.5, PROMINENT EXPRESSION OBSERVED IN DIFFERENTIATED DECIDUA. AT
 E7.5, INTENSE EXPRESSION IN EXTRAEMBRYONIC ENDODERM, AMNION AND
 NASCENT MESODERM. AT 8.5, ABUNDANT EXPRESSION IN SOWITES AND YOLK
 SAC FOLLOWED BY A COMINATION TO DERMATOTOME COMPARTMENT. BETWEEN

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FT CARBOHYD 951 951 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1016 1016 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1220 1220 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1317 1317 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1523 1523 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1711 1711 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1733 1733 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 878 915 GEYIDDHGCHOTCEASCAKCKMGPLOEDICSPVTRYVD -->
FT ATEBSWEGEGCNLVKRNKLNLCQRRVLDQLCCCKCTFQGS
FT (IN ISOFORM PCSA).
FT VARSPLIC 916 1877 MISSING (IN ISOFORM PCSA).
SQ SEQUENCE 1877 AA; 209287 MW; EGS50EADPE0EA1C3 CRC64;

Query Match 17.4%; Score 86.5; DB 1; Length 1877;
Best Local Similarity 22.1%; Pred. No. 0.37;
Matches 29; Conservative 6; Mismatches 43; Indels 53; Gaps 3;

OY 1 CSONEYFDSLHACIPCOLR---CSSNTPPLT-----COR-YCCEYFDSLHA 44
DB 1481 CAVEYWEQSGSRHCPQCKHKKSCGSEPDQCYCPRETFILNTTCVKECEGYHTKDS 1540
OY 43 -----HACPCLRCSP-----PTQYQCCFSEYFDSLHACP----- 73
DB 1541 QQCVCCHSCCTCGEPHMOCLSCRPGFQKGKCLQCRGYGEGSISGCEKDKSCK 1600
OY 74 -----PATCQ 78
DB 1601 SCRGPRPTDQ 1611

RESULT 9
KRA3_SHEEP
AC P02431; STANDARD; PRT; 131 AA.
ID KRA3_SHEEP
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1986 (Rel. 01, Last sequence update)
DT 01-AUG-1991 (Rel. 19, Last annotation update)
DE Keratin, high-sulphur matrix protein, IIA3.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
OK [1]
RN MEDLINE=74022242; Pubmed=4584026;
RX SEQUENCE.
RA Swart L.S., Haylett T.;
RT "Studies on the high-sulphur proteins of reduced Merino wool. Amino
RT acid sequence of protein SCMB-3A3."
RL Biochem. J. 133:641-654(1973).
CC -I- FUNCTION: THE KERATIN PRODUCTS OF MAMMALIAN EPIDERMAL DERIVATIVES
CC SUCH AS WOOL AND HAIR CONSIST OF MICROFIBRILS EMBEDDED IN A RIGID
CC MATRIX OF OTHER PROTEINS. THE MATRIX PROTEINS INCLUDE THE HIGH-
CC SULFUR AND HIGH-TYROSINE KERATINS, HAVING MOLECULAR WEIGHTS OF
CC 6-20 kDa. WHEREAS THE MICROFIBRILS CONTAIN THE LARGER, LOW-SULFUR
CC KERATINS (40-56 kDa).
CC -I- MISCELLANEOUS: THE SOURCE OF THIS PROTEIN IS MERINO WOOL.
DR PIR: A02840; KRHA3.
DR InterPro: IPR002494; Keratin_B2.
DR Pfam: PF01500; Keratin_B2; 1.
DR Kew Keratin.
SQ SEQUENCE 131 AA; 14163 MW; 8C0B56C0070B1C50 CRC64;

Query Match 16.7%; Score 83; DB 1; Length 131;
Best Local Similarity 25.2%; Pred. No. 0.08;
Matches 26; Conservative 12; Mismatches 35; Indels 30; Gaps 6;

OY 1 CSONEYFDSLHACIPCOLR---CSSNTPPLT-----COR-YCCEYFDSLHA 44
DB 18 CLQPPRYND-----PCCCRPVSCQTVSRPTTFVPRCRPICPERRRVCCDPSLGBC 71
OY 45 CFCLRGSPPTCOY-----CFHSEYFDSLHACP---PATCQ 79

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Db 72 CRPITCPTS:COAAVCRPCWATTCQCVSVQCCRCRPTSCOP 114

RESULT 10

| ID | UBPM_MOUSE | STANDARD; | PRT; | 526 AA. |
|--------------------------|--|-----------|------|---------|
| AC | Q61068; | | | |
| DT | 01-NOV-1997 (Rel. 35, Last sequence update) | | | |
| DT | 01-NOV-1997 (Rel. 35, Last sequence update) | | | |
| DT | 15-JUN-2002 (Rel. 41, Last annotation update) | | | |
| DE | Ubiquitin carboxyl-terminal hydrolase DUB-1 (EC 3.1.2.15) (Ubiquitin deubiquitinase DUB-1) (Ubiquitin-specific processing protease DUB-1) (Deubiquitinating enzyme 1). | | | |
| DE | DUB1 OR DUB-1. | | | |
| GN | Mus musculus (Mouse). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | |
| OX | NCBI_TaxID=10090; | | | |
| RA | SEQUENCE FROM N.A. | | | |
| RA | MEDLINE=96194957; PubMed=8622927; | | | |
| RA | Zhu Y., Carroll M., Papa F.R., Hochstrasser M., D'Andrea A.D.; | | | |
| RL | "DUB-1, a deubiquitinating enzyme with growth-suppressing activity."; | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 93:3275-3279(1996). | | | |
| CC | -1- FUNCTION: HAS GROWTH-SUPPRESSING ACTIVITY, INDUCES ARREST IN G1 PHASE UPON CONTROLLED EXPRESSION. | | | |
| CC | -1- CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)O = ubiquitin + a thiol. | | | |
| CC | -1- INDUCTION: BY INTERLEUKIN-3. | | | |
| CC | -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C19. | | | |
| CC | ----- | | | |
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| CC | ----- | | | |
| DR | EMBL; U41636; AAC52532.1; - | | | |
| DR | MEROPS; C19.031; - | | | |
| DR | MED; MGI:107659; Dnbl1. | | | |
| DR | InterPro: IPR001394; UCH-2. | | | |
| DR | Pfam; PF00442; UCH-1; 1. | | | |
| DR | Pfam; PF00443; UCH-2; 1. | | | |
| DR | PROSITE; PS00972; UCH_2_1; 1. | | | |
| DR | PROSITE; PS00973; UCH_2_2; 1. | | | |
| DR | PROSITE; PS50235; UCH_2_3; 1. | | | |
| FW | Ub1 conjugation pathway; Hydrolase; Thiol protease; Multigene family. | | | |
| FT | ACT_SITE 60 60 BY SIMILARITY. | | | |
| FT | ACT_SITE 298 298 BY SIMILARITY. | | | |
| FT | ACT_SITE 307 307 BY SIMILARITY. | | | |
| SO | SEQUENCE 526 AA; 59073 MW; 263AA7B7579694EBA CRC64; | | | |
| Query Match | 16.5%; Score 82; DB 1; Length 526; | | | |
| Best Local Similarity | 35.8%; Pred. NO. 0.33; | | | |
| Matches 19; Conservative | 8; Mismatches 18; Indels 8; Gaps 2; | | | |

FT DOMAIN 707 754 LAMININ EGF-LIKE 6.
 FT DOMAIN 755 809 LAMININ EGF-LIKE 7.
 FT DOMAIN 810 865 LAMININ EGF-LIKE 8.
 FT DOMAIN 866 916 LAMININ EGF-LIKE 9.
 FT DOMAIN 917 964 LAMININ EGF-LIKE 10.
 FT DOMAIN 965 1013 LAMININ EGF-LIKE 11.
 FT DOMAIN 1014 1071 DOMAIN II AND I.
 FT DOMAIN 1071 1141 COILED COIL (POTENTIAL).
 FT DOMAIN 1200 1229 COILED COIL (POTENTIAL).
 FT DOMAIN 1424 1504 COILED COIL (POTENTIAL).
 FT DOMAIN 1535 1579 COILED COIL (POTENTIAL).
 FT SITE 1059 1061 CELL ATTACHMENT SITE (POTENTIAL).
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 328 328 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 631 631 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 837 837 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 980 980 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1185 1185 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1518 1518 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 1587 AA; 172051 MW; 3CB6B09B5F20319 CRC64;

Query Match 16.3%; Score 81; DB 1; Length 1587;
 Best Local Similarity 31.0%; Pred. No. 1.1;
 Matches 22; Conservative 8; Mismatches 31; Indels 10; Gaps 4;

OY 12 HACICQRCNSNTPLTCQRYCEYFDSLHACPCLRC---SPPTQYCCFHEYPD 67
 Db 322 HECLPC--NCSSRSECTFDR--ELFSTGHCGRCHCRHTAGHCHERCENFYHWP 376
 OY 68 LHMCPPTCQ 78
 Db 377 RM-PCQPCDCQ 386

RESULT 12
 PAC4_RAT STANDARD; PRT; 937 AA.
 AC 063415;

DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DB Paired basic amino acid cleaving enzyme 4 precursor (EC 3.4.21.-)
 DB (Subtilisin/kexin-like protease PAC4) (Subtilisin-like proprotein
 DE convertase 4) (SPC4).

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]

SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Hypothalamus, and Pituitary;
 RX MEDLINE=94349873; PubMed=8070361;

RA Johnson R.C., Darlington D.N., Hand T.A., Bloomquist B.T., Mains R.E.;
 RT "PAC4: a subtilisin-like endoprotease prevalent in the anterior
 RT pituitary and regulated by thyroid status";
 RL Endocrinology 135:1178-1185(1994).

CC -1- FUNCTION: LIKELY TO REPRESENT AN ENDOPEPTASE ACTIVITY WITHIN THE
 CC CONSTITUTIVE SECRETORY PATHWAY, WITH UNIQUE RESTRICTED
 CC DISTRIBUTION IN BOTH NEUROENDOCRINE AND NON-NEUROENDOCRINE TISSUES
 CC AND CAPABLE OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF.

CC -1- CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR
 CC PROPOTERINS BY CLEAVAGE OF ARG-XAA-YAA-ARG-|-ZAA BONDS,
 CC WHERE XAA CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.

CC -1- COFACTOR: PROBABLY CALCIUM-DEPENDENT (BY SIMILARITY).

CC -1- TISSUE SPECIFICITY: HIGH EXPRESSION IN THE ANTERIOR PITUITARY AND
 CC IN SEVERAL BRAIN REGIONS, THE ATRIUM, AND THE VENTRICLE.

CC -1- DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE
 CC ASSISTING THE FOLDING OF THE ZMOGEN WITHIN THE ENDOPLASMIC
 CC RETICULUM.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.

CC -1- SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.

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DR EMBL; L31894; AAA61987.1; -.
 DR HSPB; Q99405; IMP1.

DR MEROPS; S08.075; -.
 DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR002174; Furin-like.
 DR InterPro; IPR002884; P domain.

DR InterPro; IPR000209; Peptidase_S8.
 DR Pfam; PF00082; Peptidase_S8; 1.

DR Pfam; PF01483; P; PARTIAL.
 DR PRINTS; PR00723; SUBTILISIN.

DR ProDom; PD000717; P domain; 1.
 DR SMART; SM00181; EGF_1.

DR SMART; SM00261; FU; 5.
 DR PROSITE; PS00136; SUBTILASE ASP; 1.

DR PROSITE; PS00137; SUBTILASE HIS; 1.
 DR PROSITE; PS00138; SUBTILASE SER; 1.

KW Hydrolyase; Serine protease; Glycoprotein; Zymogen; Signal; Calcium;
 KW Cleavage on pair of basic residues; Repeat.

FT SIGNAL 1 45
 FT PROPEP 46 132
 FT CHAIN 133 937

FT DOMAIN 133 454
 FT DOMAIN 477 615
 FT DOMAIN 680 937

FT SITE 132 133
 FT SITE 534 536
 FT ACT_SITE 186 186

FT ACT_SITE 227 227
 FT ACT_SITE 401 401
 FT CARBOHYD 240 240

FT CARBOHYD 882 882
 FT CARBOHYD 900 900
 SQ SEQUENCE 937 AA; 104053 MW; F386557C33705C8 CRC64;

Query Match 16.2%; Score 80.5; DB 1; Length 937;
 Best Local Similarity 24.4%; Pred. No. 0.76;
 Matches 30; Conservative 9; Mismatches 39; Indels 45; Gaps 6;

OY 1 CSQNYFDSLHACPCLRC-----SNTPPLTCOR--YCCEYFDSLHACP----- 46
 Db 701 CPLGTFDPTARRCRCKGCTCTGSRPTQCLSCRGFTYHQTNTCVTLCPAGLVAD 760

OY 47 ----CLRCSPPTCQYC-----CFHSEYFDSLHACPPTCQ 78
 Db 761 SQRCLRGH-PSQCKVDPEKSTVCKEGLANGSCIPDCPEPTGYFDSLIRC--GECH 817

OY 79 PYC 81
 Db 818 HTC 820

RESULT 13
 LMB2_HUMAN STANDARD; PRT; 1798 AA.
 AC P55268; Q16321;

DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DB Laminin beta-2 chain precursor (S-laminin) (laminin B1s chain).

GN LAMB2 OR LAMS.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;


```

FT  CONFLICT  914  914  R -> G (IN REF. 2).
FT  CONFLICT  1179 1179  G -> A (IN REF. 2).
SQ  SEQUENCE  1798 AA; 196079 MW; 9555CF5B24850CB7 CRC64;

Query Match
Best Local Similarity 16.2%; Score 80.5; DB 1; Length 1798;
Matches 29; Conservative 7; Mismatches 31; Indels 41; Gaps 8;

Qy  1 CSQNEPDSL------HACIP-----COL-RCSSNTPPLTCORYCC 35
Db  943 CHQEGYSGQIVCHFRAGYTGRCACAGHFGDPSPGRGQLGSCSGNIDMPDPD--AC 1000
Qy  36 EYFDSLHACPLAC-----SPTCYC--CHSEYFDSLHACPPATC 77
Db  1001 D-----PHTGQLRLCHHTBEGPHCMCKPFGQAPAROSCHRC--TC 1040

RESULT 14
LMA1_HUMAN STANDARD; PRT; 3075 AA.
ID  LMA1_HUMAN
AC  P25391;
DT  01-MAY-1992 (Rel. 12, Created)
DT  01-MAY-1992 (Rel. 12, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Laminin alpha-1 chain precursor (Laminin A chain).
GN  LMA1 OR LAMA.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX  NCBI_TaxId=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=9133420; PubMed=1714537;
RA  Haepparaanta T., Uitto J., Ruoslahti E., Engvall E.;
RT  "Molecular cloning of the cDNA encoding human laminin A chain.";
RL  Matrix 11:151-160(1991).
RN  [2]
RP  SEQUENCE OF 1-2628 FROM N.A.
RX  MEDLINE=91264789; PubMed=2049067;
RA  Nissen M., Vuolteenaho R., Booc-Handford R., Kallunki P.,
RT  Tytgvaeson K.;
RT  "Primary structure of the human laminin A chain. Limited expression
RT  in human tissues.";
RL  Biochem. J. 276:369-379(1991).
RN  [3]
RP  SEQUENCE OF 2397-3072 FROM N.A.
RX  MEDLINE=89280632; PubMed=2733383;
RA  Olsen D., Nagayoshi T., Fazio M., Peltonen J., Jaakkola S.,
RA  Sanborn D., Sasaki T., Kivianleml H., Chu M.L., Deutmann R.,
RA  Timpl R., Uitto J.;
RT  "Human laminin: cloning and sequence analysis of cDNAs encoding A, B1
RT  and B2 chains, and expression of the corresponding genes in human
RT  skin and cultured cells.";
RL  Ldb. Invest. 60:772-782(1989).
RN  [4]
RP  FUNCTION: Binding to cells via a high affinity receptor, laminin
RN  is thought to mediate the attachment, migration, and organization
RN  of cells into tissues during embryonic development by interacting
RN  with other extracellular matrix components.
CC  -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC  different polypeptide chains (alpha, beta, gamma), which are bound
CC  to each other by disulfide bonds into a cross-shaped molecule
CC  comprising one long and three short arms with globules at each
CC  end.
CC  THE ALPHA-1 CHAIN IS A SUBUNIT OF LAMININ-1 (BHS LAMININ) AND
CC  LAMININ-3 (S-LAMININ).
CC  -1- SUBCELLULAR LOCATION: Extracellular.
CC  -1- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR
CC  COMPONENT).
CC  -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
CC  WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC  -1- DOMAIN: DOMAINS VI, IV AND G ARE GLOBULAR.
CC  -1- SIMILARITY: CONTAINS 17 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
CC  -1- SIMILARITY: CONTAINS 17 LAMININ EGF-LIKE DOMAINS.

CC  -1- SIMILARITY: CONTAINS 2 LAMININ DOMAINS IV.
CC  -1- SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.
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CC  EMBL: X58531, CAA1418.1; -.
CC  PIR: S14458; S14458.
CC  HSP: Q60675; IQU0.
CC  Genew: HGNC:6481; LAMA1.
CC  MIM: 150320; -.
CC  InterPro: IPR000561; EGF-like.
CC  InterPro: IPR001886; LamNT.
CC  InterPro: IPR000034; Laminin_B.
CC  InterPro: IPR002049; Laminin_EGF.
CC  InterPro: IPR001791; Laminin_G.
CC  Pfam: PF00052; Laminin_B; 2.
CC  Pfam: PF00054; Laminin_G; 5.
CC  Pfam: PF00055; Laminin_Nterm; 1.
CC  PRINTS: PR00011; EGF_LAMININ.
CC  ProDom: PD002082; LamNT; 1.
CC  ProDom: PD003031; Laminin_B; 2.
CC  SMART: SM00180; EGF_Lam; 14.
CC  SMART: SM00001; EGF_Like; 1.
CC  SMART: SM00281; Lamb; 2.
CC  SMART: SM00282; LamG; 5.
CC  SMART: SM00136; LamNT; 1.
CC  PROSITE: PS00023; EGF_1; 11.
CC  PROSITE: PS01186; EGF_2; 2.
CC  PROSITE: PS01248; LAMININ_TYPE_EGF; 15.
CC  PROSITE: PS50025; LAM_G_DOMAIN; 5.
CC  KX Glycoprotein, Basement membrane; Extracellular matrix; Coiled coil;
CC  Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
CC  FT SIGNAL 1 17
CC  FT CHAIN 18 3075
CC  FT DOMAIN 18 269 LAMININ N-TERMINAL (DOMAIN VI).
CC  FT DOMAIN 270 326 LAMININ EGF-LIKE 1.
CC  FT DOMAIN 327 396 LAMININ EGF-LIKE 2.
CC  FT DOMAIN 397 453 LAMININ EGF-LIKE 3.
CC  FT DOMAIN 454 502 LAMININ EGF-LIKE 4.
CC  FT DOMAIN 503 512 LAMININ EGF-LIKE 5 (N-TERMINAL).
CC  FT DOMAIN 517 708 LAMININ DOMAIN IV 1 (DOMAIN IV B).
CC  FT DOMAIN 709 741 LAMININ EGF-LIKE 6.
CC  FT DOMAIN 742 790 LAMININ EGF-LIKE 7.
CC  FT DOMAIN 791 848 LAMININ EGF-LIKE 8.
CC  FT DOMAIN 849 901 LAMININ EGF-LIKE 9.
CC  FT DOMAIN 902 950 LAMININ EGF-LIKE 10.
CC  FT DOMAIN 951 997 LAMININ EGF-LIKE 11.
CC  FT DOMAIN 998 1043 LAMININ EGF-LIKE 12.
CC  FT DOMAIN 1044 1089 LAMININ EGF-LIKE 13.
CC  FT DOMAIN 1090 1149 LAMININ EGF-LIKE 14.
CC  FT DOMAIN 1150 1159 LAMININ EGF-LIKE 15.
CC  FT DOMAIN 1160 1361 LAMININ DOMAIN IV 2 (DOMAIN IV A).
CC  FT DOMAIN 1362 1402 LAMININ EGF-LIKE 14 (C-TERMINAL).
CC  FT DOMAIN 1403 1451 LAMININ EGF-LIKE 15.
CC  FT DOMAIN 1452 1508 LAMININ EGF-LIKE 16.
CC  FT DOMAIN 1509 1555 LAMININ EGF-LIKE 17.
CC  FT DOMAIN 1556 1566 LAMININ II AND I.
CC  FT DOMAIN 1567 2297 LAMININ G-LIKE 1.
CC  FT DOMAIN 2117 2297 LAMININ G-LIKE 2.
CC  FT DOMAIN 2305 2481 LAMININ G-LIKE 3.
CC  FT DOMAIN 2486 2673 LAMININ G-LIKE 4.
CC  FT DOMAIN 2713 2885 LAMININ G-LIKE 5.
CC  FT DOMAIN 2890 3070 LAMININ G-LIKE 5.
CC  FT DOMAIN 1706 1796 COILED COIL (POTENTIAL).
CC  FT DOMAIN 1968 1989 COILED COIL (POTENTIAL).
CC  FT DOMAIN 2088 2120 COILED COIL (POTENTIAL).
CC  FT DOMAIN 2534 2536 CELL ATTACHMENT SITE.

```


Sat Feb 8 14:52:32 2003

us-09-854-864-13.rsp

Page 13

| | | | | |
|----|----------|---------|------------|-------------------------|
| FT | REPEAT | 611 | 644 | 7. |
| SQ | SEQUENCE | 965 AA; | 108494 MW; | 121C57BB07C6FA9D CRC64; |

| | | | | |
|--------------------------|--------|-----------------|------------|-------------|
| Query Match | 16.0%; | Score 79.5; | DB 1; | Length 965; |
| Best Local Similarity | 29.6%; | Pred. No. 0.98; | | |
| Matches 29; Conservative | 6; | Mismatches 26; | Indels 37; | Gaps 7; |

QY 12 HACT-PCQGLRCSSTNPTLTQRYC-----CEYFDSLHAAPC-----LRCSF--P 53
 | : | | | | | | | | | | : |
 Db 456 HICLKPCNLTLSGHH--KCGKCKHPGKCPCLSDSDNDLVCPGNTVVPAPVRCGTKLP 513

```

QY      54 TCQYCCF-----HEYFDSLHACPPAT 76
      || : |      | : | | |
Db      514 TCNHPCLIKVVGESTCGHKMPHTCH--SLDVSACPCT 549

```

```
Search completed: February 4, 2003, 12:58:09
Job time : 8.5749 secs
```


GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 4, 2003, 12:56:21 ; Search time 9.51012 Seconds
(without alignments)
818.800 Million cell updates/sec

Title: US-09-854-864-13

Perfect score: 498
Sequence: 1 CSQNEYFDSLHACIPCOLR.....SEYFDSLHACPPATCPYRC 81

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:
2: p1r2:
3: p1r3:
4: p1r4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 201 | 40.4 | 184 | 2 S43486 | B-cell maturation |
| 2 | 94.5 | 19.0 | 223 | 2 B38346 | ultra-high-sulfur |
| 3 | 94.5 | 19.0 | 230 | 2 A38346 | ultra-high-sulfur |
| 4 | 92.5 | 18.6 | 169 | 1 S18946 | ultra-high-sulfur |
| 5 | 91.5 | 18.4 | 186 | 2 A45910 | ultra-high-sulfur |
| 6 | 89 | 17.9 | 1574 | 2 T13954 | MEGF6 protein - ra |
| 7 | 87 | 17.5 | 1680 | 2 A43434 | furin (EC 3.4.21.7 |
| 8 | 86.5 | 17.4 | 1548 | 2 S34583 | serine proteinase |
| 9 | 86 | 17.3 | 188 | 2 JG6547 | high sulfur protei |
| 10 | 83 | 16.7 | 131 | 1 KRSH3 | keratin high-sulfu |
| 11 | 83 | 16.7 | 175 | 2 S37649 | high-sulfur kerati |
| 12 | 82 | 16.5 | 126 | 2 I46489 | cysteine-rich hair |
| 13 | 82 | 16.5 | 526 | 2 JG6133 | deubiquitinating e |
| 14 | 81 | 16.3 | 2823 | 2 T23064 | hypothetical prote |
| 15 | 81 | 16.3 | 2823 | 2 T23064 | protein T22A3.8 (i |
| 16 | 81 | 16.3 | 3102 | 2 T43291 | laminin alpha chai |
| 17 | 80.5 | 16.2 | 151 | 2 S60314 | hair Keratin cyste |
| 18 | 80.5 | 16.2 | 937 | 2 I53282 | gene PACE4 protein |
| 19 | 80.5 | 16.2 | 1101 | 2 T16840 | hypothetical prote |
| 20 | 80.5 | 16.2 | 1798 | 2 S53869 | laminin beta-2 cha |
| 21 | 80 | 16.1 | 3075 | 2 S14458 | laminin alpha-1 ch |
| 22 | 79.5 | 16.0 | 965 | 2 S62935 | hypothetical prote |
| 23 | 79.5 | 16.0 | 1077 | 2 T41146 | probable cysteine- |
| 24 | 79.5 | 16.0 | 3133 | 2 S52093 | hemocytin - silkw |
| 25 | 79 | 15.9 | 861 | 2 A48825 | Norch homolog Mork |
| 26 | 78.5 | 15.8 | 201 | 2 D71190 | hypothetical prote |
| 27 | 78.5 | 15.8 | 294 | 2 T23682 | hypothetical prote |
| 28 | 78 | 15.7 | 572 | 2 T29880 | hypothetical prote |
| 29 | 78 | 15.7 | 1188 | 2 D86236 | protein F14N23.5 (|

| | | | | | |
|----|------|------|------|----------|--------------------|
| 30 | 77.5 | 15.6 | 132 | 1 KRGT3J | keratin high-sulfu |
| 31 | 77.5 | 15.6 | 177 | 2 S37650 | high-sulfur kerati |
| 32 | 77 | 15.5 | 162 | 2 I47107 | high-sulfur wool m |
| 33 | 77 | 15.5 | 172 | 1 KRSH3 | keratin high-sulfu |
| 34 | 77 | 15.5 | 5376 | 2 T42215 | zonadhesin - mouse |
| 35 | 76.5 | 15.4 | 932 | 2 I52527 | PACE4A - mouse (fr |
| 36 | 76.5 | 15.4 | 1513 | 2 T23681 | hypothetical prote |
| 37 | 76.5 | 15.4 | 2414 | 2 A54277 | transcription adap |
| 38 | 76 | 15.3 | 182 | 2 I47105 | high-sulfur wool m |
| 39 | 76 | 15.3 | 172 | 2 I47105 | high-sulfur wool m |
| 40 | 76 | 15.3 | 1299 | 2 T43251 | furin (EC 3.4.21.7 |
| 41 | 76 | 15.3 | 2440 | 2 S39162 | transcription coac |
| 42 | 76 | 15.3 | 2441 | 2 S39161 | CRFB-binding prote |
| 43 | 76 | 15.3 | 2910 | 2 T42214 | ocogelin - mouse |
| 44 | 75.5 | 15.2 | 654 | 2 T30136 | hypothetical prote |
| 45 | 75.5 | 15.2 | 1713 | 2 A55347 | adhesive ligand ep |

ALIGNMENTS

RESULT 1
S43486
B-cell maturation factor - human
N/Alternate names: BCM protein; BCM protein; BCL protein
C/Species: Homo sapiens (man)
C/Date: 27-Jan-1995 #sequence revision 27-Jan-1995 #text_change 21-Jul-2000
A/Accession: S43486; S31208; S35661
R/Laabi, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.
Nucleic Acids Res. 22, 1147-1154, 1994
A/Title: The BCM gene, preferentially expressed during B lymphoid maturation, is bidire
A/Reference number: S43486; MUID:94218335; PMID:8165126
A/Accession: S43486
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-184 <LAA>
A/Cross-references: EMBL:Z14954; NID:G29407; PIDN:CA78679.1; PID:G29408
A/Reference number: S31208; MUID:93010984; PMID:1396583
A/Accession: S31208
A/Molecule type: mRNA
A/Residues: 1-184 <LAA>
A/Cross-references: EMBL:Z14955
C/Genetics:
A/Genes: GDB:BCM
A/Cross-references: GDB:135977; OMIM:109545
A/Map position: 16p13.1-16p13.1
A/Introns: 44/1; 93/1
C/Superfamily: human B-cell maturation factor

Query Match 40.4%; Score 201; DB 2; Length 184;
Best local Similarity 100.0%; Pred. No. 8.1e-11;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSNTPPTCORYC 34
DB 8 CSQNEYFDSLHACIPCOLRCSNTPPTCORYC 41

RESULT 2
B38346
ultra-high-sulfur keratin 2 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 31-Mar-1992 #sequence revision 31-Mar-1992 #text_change 24-Sep-1999
A/Accession: A38600; B38346
R/Wood, L.; Mills, M.; Hatzenbuehler, N.; Vogeli, G.

J. Biol. Chem. 266, 4024, 1991
A>Title: Serine-rich ultra high sulfur protein gene expression in murine hair and skin c
A:Reference number: A38660; MUID:91154184; PMID:1840598
A:Accession: A38660
A:Molecule type: DNA
A:Residues: 1-223 <MO3>
A:Cross-references: GB:M37760; NID:G200963; PIDN:AAA40107.1; PID:G200964
A>Note: This is a correction
R:Wood, L.; Mills, M.; Hattenhuber, N.; Vogel, G.
J. Biol. Chem. 265, 21375-21380, 1990
A>Title: Serine-rich ultra high sulfur protein gene expression in murine hair and skin c
A:Reference number: A38346; MUID:91065960; PMID:2250030
A:Accession: B38346
A:Molecule type: DNA
A:Residues: 1-21, 'GGCGSGCGGCAGCGCGSSCKEVC', 22-40, 'GSS', 44-45, 'G', 47-48, 'S', 50, 'GSS',
<MOO>
A:Cross-references: GB:M37759; NID:G200961; PIDN:AAA40106.1; PID:G200962
A>Note: The sequence reported in this paper has been corrected. See A38660
C:Superfamily: ultra-high-sulfur keratin

[illegible]

```

RESULT 3
A38346
ultra-high-sulfur keratin 1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 24-Sep-1999
C:Accession: A38346
R:Wood, L.; Miller, M.; Hatzenbuehler, N.; Vogel, G.
J. Biol. Chem. 265, 21375-21380, 1990
A:Title: Serine-rich ultra high sulfur protein gene expression in murine hair and skin
A:Reference number: A38346; MUID:9106560; PMID:2250030
A:Accession: A38346
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-230 <MOO>
A:Cross-references: GB:M7759; NID:g200961; PIDN:AAA40106.1; PID:g200962
C:Superfamily: ultra-high-sulfur keratin

```

| Query Match | Similarity | Score | DB | Length |
|------------------|------------|-----------------|----|-----------------------------------|
| Best Local Match | 29.6% | Pred. No. 0.15; | | |
| Matched | 24; | Conservative | 3; | Mismatches 27; Indels 27; Gaps 5; |

RESULT 4
S18946
ultra high-sulfur keratin 1 - human
N/Alternate names: UHS keratin, ultra high-sulfur matrix protein
C/Species: Homo sapiens (man)
C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #next_change 22-Oct-1999
C/Accession: S18946; B36686
R/Draabert, B.; Doenneke, D.
submitted to the EMBL Data Library, December 1991
./description: Nucleotide sequence of a Human high-sulfur keratin cDNA.

A:Reference number: S18946
A:Accession: S18946
A:Molecule type: mRNA
A:Residues: 1-169 <DRA>
A:Cross-references: EMBL:X63755; NID:G32471; PIDN:CAA45283.1; PID:G32472
J:MacKinnon, P.J.; Powell, B.C.; Rogers, G.E.
J: Cell Biol. 111, 2587-2600, 1990
A:Title: Structure and expression of genes for a class of cyteine-rich proteins of the
A:Reference number: A36686; MUID:91115951; PMID:1703541
A:Accession: B36686
A:Molecule type: DNA
A:Residues: 1-39, 'Y', 41-169 <MAC>
A:Cross-references: GB:X55293; NID:G34078; PIDN:CAA39005.1; PID:G34079
C:Genetics:
A:Gene: GDB:XRN1
A:Cross-references: GDB:125257; OMIM:148021
A:Map position: 11q13-11q13
C:Superfamily: ultra-high-sulfur keratin
C:Keywords: hair; tandem repeat
F:7-15/Region: Ser-rich nonapeptide repeat
F:59-68/Region: Gly-rich decapeptide repeat
F:69-78/Region: Gly-rich decapeptide repeat
F:79-88/Region: Cys-rich decapeptide repeat
F:89-97/Region: Ser-rich nonapeptide repeat
F:98-107/Region: Cys-rich decapeptide repeat
F:108-117/Region: Cys-rich decapeptide repeat
F:118-126/Region: Ser-rich decapeptide repeat
F:127-136/Region: Cys-rich decapeptide repeat
F:137-145/Region: Ser-rich nonapeptide repeat
F:146-155/Region: Cys-rich decapeptide repeat
F:156-165/Region: Cys-rich decapeptide repeat

Query Match 18.6%; Score 92.5; DB 1; Length 169;
 Best Local Similarity 30.0%; Pred. No. 0.18;
 Matches 27; Conservative 5; Mismatches 37; Indels 21; Gaps 5

```

OY      1 CSQNYFSLHACIPQQLRCSNPTLQRYGCEYFDSLHAC-PCR-----CS 51
DB      77 CSQ-----CSCKPFC--CSGGGSCCQSCCKPFCSCCKPFCSSGRRSSCCQ 127
OY      52 PPTQYCCFHSBYFDSLHACPPATCPYC 81
DB     128 SSCKPCCSSGGGSS---CCQSCCKPFC 154

```

RESULT 5
A45910
ultra-high-sulfur keratin - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 24-Sep-1999
C:Accession: A45910
R:McNab, A.R.; Wood, L.; Thieriault, N.; Gierman, T.; Vogel, G.
J. Invest. Dermatol. 92, 263-266, 1989
A:Title: An ultra-high sulfur keratin gene is expressed specifically during hair growth
A:Reference number: A45910; MUID:89140394; PMID:2465353
A:Accession: A45910
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-186 <MCN>
A:Cross-references: GB:M27665; NID:g341749; PIDN:AAA81560.1; PID:g1066818
i:Superfamily: ultra-high-sulfur keratin

| | Query Match | Similarity | Score | DB | Length |
|------------|-------------|--------------|-------|------------|--------|
| Best Local | 25 | 34.7% | 91.5 | 2 | 186 |
| Matches | 25 | Conservative | 4 | Mismatches | 24 |
| | | | | Indels | 19 |
| | | | | Gaps | 6 |

| Qy | 14 | CIP--COLRC--SSNTPITCQRCCEYFDSLHAC--PCLRCSPRCQYCCFHSEYFDSL | 69 |
|----|----|---|-----|
| | | : : : : | |
| Db | 85 | CQPCQPSCCSSCCQPRCCSSCCQPRCISCCQPC--CRPSCCQSSC----- | 132 |

| Qy | 70 | HACPPATCQPC 81 |
|----|-----|------------------|
| | | |
| Db | 133 | --CRPC--CQPC 141 |

A:Experimental source: clone T22A3

C:Genetics:

A:Gene: CESP:T22A3.8

A:Map position: 1

A:Introns: 45/1; 282/2; 312/3; 416/2; 1255/3; 1329/3; 1418/3; 1776/2; 1988/2; 2760/2

C:Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h

Query Match 16.3%; Score 81; DB 2; Length 2823;

Best Local Similarity 27.7%; Pred. No. 14;

Matches 26; Conservative 10; Mismatches 32; Indels 26; Gaps 7;

Qy 1 CSQNEYFDSLHACIPCOLRCSSNTPPL---TCQRYCCYFDSLHACPLRC-----SPP 53

Db 873 CSDGFEDPLTGKCIETC---TCNGNIDPMGIGNC-----DS--ETGKCLKICIGHTGD 920

Qy 54 TCQYCCFHSYFDSLHACPPATC-----QPYC 81

Db 921 SCESCKEH-HWGNAQLHTCKPCGCHTQGVNPOC 953

RESULT 15

F87908

protein T22A3.8 [imported] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-Aug-2001

C:Accession: F87908; E87908

R:anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog

A:Reference number: A75000; MUID:93069613; PMID:9851916

A>Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C_ele

A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A:Accession: F87908

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-2823 <STO>

A:Cross-references: GB:chr_1; PIDN:CAA15432.1; PID:g3924779; GSPDB:GN00019; CESP:T22A3.8

A:Accession: E87908

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-2823 <ST2>

A:Cross-references: GB:chr_1; PIDN:CAB03385.1; PID:g3924881; GSPDB:GN00019; CESP:T22A3.8

C:Genetics:

A:Gene: T22A3.8

A:Map position: 1

C:Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h

Query Match 16.3%; Score 81; DB 2; Length 2823;

Best Local Similarity 27.7%; Pred. No. 14;

Matches 26; Conservative 10; Mismatches 32; Indels 26; Gaps 7;

Qy 1 CSQNEYFDSLHACIPCOLRCSSNTPPL---TCQRYCCYFDSLHACPLRC-----SPP 53

Db 873 CSDGFEDPLTGKCIETC---TCNGNIDPMGIGNC-----DS--ETGKCLKICIGHTGD 920

Qy 54 TCQYCCFHSYFDSLHACPPATC-----QPYC 81

Db 921 SCESCKEH-HWGNAQLHTCKPCGCHTQGVNPOC 953

Search completed: February 4, 2003, 12:59:45
Job time : 12.5101 secs

RESULT 6

T13954
MEGF6 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C:Accession: T13954
R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A:Reference number: 214126; MUID:98360089; PMID:9693030
A:Accession: T13954
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1574 <NAK>
A:Cross-references: EMBL:AB011532; NID:G3449293; PIDN:BAA32462.1; PID:G3449294
A:Experimental source: strain Sprague-Dawley; brain
C:Genetics:
A:Gene: MEGF6

Query Match 17.9%; Score 89; DB 2; Length 1574;
Best Local Similarity 29.4%; Pred. No. 1.8;
Matches 30; Conservative 9; Mismatches 25; Indels 38; Gaps 8;
Qy 1 CSONEYFDSLHACIPCOL-----RCSNTPLT-----CQRYCCEY-----FDSLHACPC 47
Db 966 CSAGAPCDAVTGSCI-CPAGRWPRCAQSCPLPLTGLNCSQICTCFNGASCDSVTGQC-- 1022
Qy 48 LRCSF-----PTQYCCFHSEYFDSLHACPPA-----TCQPYC 81
Db 1023 -HCAPGMWGPTC-----LQACPPGLYKKNQCHSC 1050

RESULT 7

A43434
furin (EC 3.4.21.75) 2 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Mar-2000
C:Accession: A43434
R:Roebroek, A.J.; Creemers, J.W.; Pauli, I.G.; Kurzik-Dumke, U.; Rentrop, M.; Gateff, E.
J. Biol. Chem. 267, 17208-17215, 1992
A:Title: Cloning and functional expression of Dfurin2, a subtilisin-like proprotein proc
A:Reference number: A43434; MUID:92381036; PMID:1512259
A:Accession: A43434
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1680 <ROE>
A:Cross-references: GB:M94375; NID:G157461; PID:G157462
A:Note: sequence extracted from NCBI backbone (NCBIN:111933, NCBIP:111934)
C:Genetics:
A:Gene: FlyBase:Fur2
A:Cross-references: FlyBase:FBgn0004598
C:Superfamily: subtilisin homology
C:Keywords: hydrolase; serine proteinase; transmembrane protein
F:409-652/Domain: subtilisin homology <SBT>
F:418,638/Active site: Asp, His, Ser #status predicted

Query Match 17.5%; Score 87; DB 2; Length 1680;
Best Local Similarity 25.0%; Pred. No. 2.9;
Matches 31; Conservative 12; Mismatches 31; Indels 50; Gaps 9;

Qy 1 CSONEYFDSLHACIPCOLRCSNTPLTQ-----RYC--CEYFDSLH-----ACP--- 46
Db 1051 CPDGVFENSRNRTVCPCPNCAS-----CQHPFYCTSCDH-HLVMEHKCYACPLDT 1103
Qy 47 -----CLRCSPTQCYC--CFHSEYF--DSLHACPPA-----TC 77
Db 1104 YETEDNKAFCCHCATCNGTDDCITCRSSRYAWQNKCLISCPDGFYADKKRLCQPC 1163
Qy 78 QPYC 81
Db 1164 QEGC 1167

RESULT 8

S34583
serine proteinase (EC 3.4.21.-) PC6B - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C:Accession: S34583
R:Nakagawa, T.; Murakami, K.; Nakayama, K.
FEBS Lett. 327, 165-171, 1993
A:Title: Identification of an isoform with an extremely large Cys-rich region of PC6, a
A:Reference number: S34583; MUID:93327934; PMID:8335106
A:Accession: S34583
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1548 <NAK>
A:Cross-references: GB:D17583; NID:G407344; PIDN:BAA04507.1; PID:dl005033; PID:G440374
C:Keywords: hydrolase; serine proteinase

Query Match 17.4%; Score 86.5; DB 2; Length 1548;
Best Local Similarity 22.1%; Pred. No. 3;
Matches 29; Conservative 6; Mismatches 43; Indels 53; Gaps 3;
Qy 1 CSONEYFDSLHACIPCOLRCSNTPLTQRYCCEYFDSL----- 42
Db 1152 CAAVEYWDGSHRCQPCCHKKSCGSPSEDQCYTCPRFTLLNTTCVKECEGYYHTDKDS 1211
Qy 43 -----HACPCLCRSP-----PTQYCCFHSEYFDSLHACP----- 73
Db 1312 QCVLCHSSCRTCEGPHSMQCLSCRPGWFLGKGLLQCRDGYGYGSESTSGRCEKCKSK 1271
Qy 74 -----PATCQ 78
Db 1272 SCGRPRPTDQ 1282

RESULT 9

JC6547
high sulfur protein B2E - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jul-2000
C:Accession: JC6547
R:Mitsui, S.; Ohuchi, A.; Adachi-Yamada, T.; Hotta, M.; Tsuboi, R.; Ogawa, H.
Gene 208, 123-129, 1998
A:Title: Structure and hair follicle-specific expression of genes encoding the rat high
A:Reference number: JC6547; MUID:98201605; PMID:9524245
A:Accession: JC6547
A:Molecule type: DNA
A:Residues: 1-188 <MIT>
A:Cross-references: DDBJ:AB003753; NID:G3046870; PIDN:BAA25573.1; PID:G3046871
C:Comment: This protein is a cysteine-rich, keratin associated protein.
C:Genetics:
A:Gene: b2E
C:Superfamily: keratin high-sulfur matrix protein IIIA
C:Keywords: hair

Query Match 17.3%; Score 86; DB 2; Length 188;
Best Local Similarity 22.5%; Pred. No. 0.73;
Matches 23; Conservative 10; Mismatches 28; Indels 62; Gaps 7;

Qy 1 CSONEYFDSLHACIP-----CQLRCSNTPLTQ-----R 32
Db 69 CSQSS-----CCQPSCCQTCQPTCCQNS---SCQSCCGTSGQSGSGGATSCVR 118
Qy 33 YC---CEYFDSLHACLCRCSPPTC-----QYCCFHSYFDSLHAC 72
Db 119 WCRPDCRVEGTCLPPCCWVSCPTPTCCQLHQAQACCRPSYCGQSCCRPA-----CCCHCC 174
Qy 73 PPATCQPYC 81
Db 175 EPSCSKPSC 183

RESULT 10
KSH3A3
keratin high-sulfur matrix protein IIIA3 - sheep
N:Alternate names: M2.6 protein
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 16-Aug-1996
C:Accession: A02840
R:Swart, L.S.; Haylett, T.
Biochem. J. 133, 641-654, 1973
A:Title: Studies on the high-sulfur proteins of reduced merino wool. Amino acid sequence
A:Reference number: A90269; MUID:74022242; PMID:4584026
A:Accession: A02840
A:Molecule type: protein
A:Residues: 1-131 <SWA>
A:Experimental source: Merino wool
C:Comment: Wool and hair consist of microfibrils embedded in a rigid matrix of other proteins
C:Superfamily: keratin high-sulfur matrix protein IIIA
C:Keywords: duplication; hair

Query Match 16.7%; Score 83; DB 1; Length 131;
Best Local Similarity 25.2%; Pred. No. 1;
Matches 26; Conservative 12; Mismatches 35; Indels 30; Gaps 6;

QY 1 CSQNEYFDSLHACIPCOLR---CSSNTPLT-----COR-YCFYFDSLHHA 44
DB 18 CLQPRYRD-----PCCRPVSCQVSRPVTFVPRCTRPICPCRRPVCCDPCSLQEGC 71

QY 45 CFCCLRCSPPTCQY-----CCFHFSEYFDSLHACP---PATCQP 79
DB 72 CRPTCCPTSCQAVGRCPCWATTCQPVSVQCPCCRPRTSCQP 114

RESULT 11
S37649
high-sulfur keratin - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
C:Accession: S37649
R:Zhunabeva, B.D.; Gening, L.V.; Gazaryan, K.G.
Mol. Biol. 26, 550-555, 1992
A:Title: Cloning and structural characterization of human hair sulfur-rich keratin genes
A:Reference number: S37649
A:Accession: S37649
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-175 <ZHU>
A:Cross-references: EMBL:X63338; NID:G311881; PIDN:CAA44938.1; PMID:G311882
C:Superfamily: keratin high-sulfur matrix protein IIIA

Query Match 16.7%; Score 83; DB 2; Length 175;
Best Local Similarity 32.4%; Pred. No. 1.3;
Matches 22; Conservative 6; Mismatches 24; Indels 16; Gaps 5;

QY 17 CQLRCSSNTPLTCQRYCCEYFDSLHACPLRCSPPTCQ--YCCF-HSEYFDSLHACP 73
DB 25 CQPSCCETS---CCQPSCE-----TSC---CQPSCCQTSFCDLFLASQLVDLSLCCQ 71

QY 74 PATCQPYC 81
DB 72 PSCCETSC 79

RESULT 12
I46489
cysteine-rich hair keratin associated protein - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 24-Sep-1999
C:Accession: I46489; S49201
R:Powell, B.C.; Arthur, J.; Nesci, A.
Differentiation 58, 227-232, 1995
A:Title: Characterization of a gene encoding a cysteine-rich keratin associated protein
A:Reference number: I46489; MUID:95228955; PMID:7536172
A:Accession: I46489

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-126 <POW>

A:Cross-references: EMBL:X80035; NID:G510540; PIDN:CAA56339.1; PID:G510541

C:Genetics:

A:Gene: KAP4L

C:Superfamily: ultra-high-sulfur keratin